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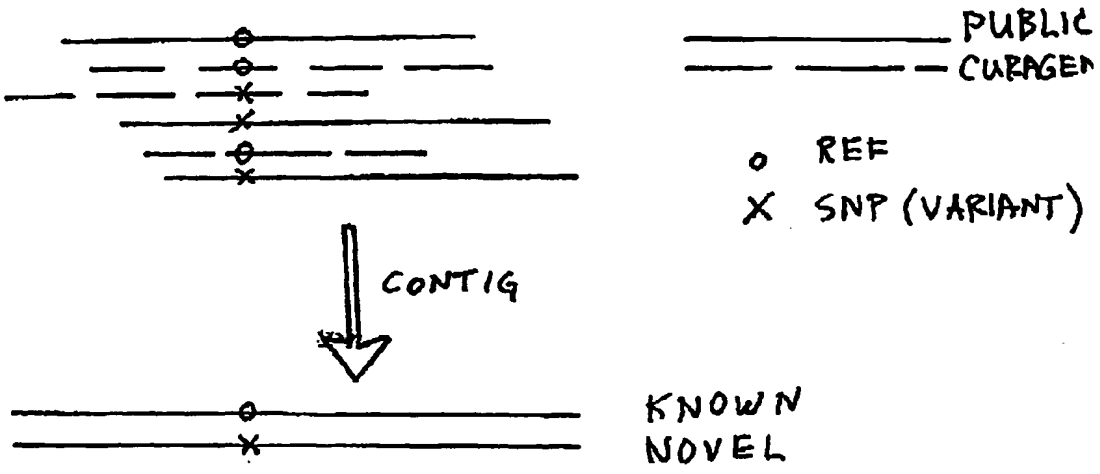
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(54) Title: NUCLEIC ACIDS CONTAINING SINGLE NUCLEOTIDE POLYMORPHISMS AND METHODS OF USE THEREOF



(57) Abstract: The invention provides nucleic acids containing single-nucleotide polymorphisms identified for transcribed human sequences, as well as methods of using the nucleic acids.

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NUCLEIC ACIDS CONTAINING SINGLE NUCLEOTIDE POLYMORPHISMS AND METHODS OF USE THEREOF

BACKGROUND OF THE INVENTION

Sequence polymorphism-based analysis of nucleic acid sequences can augment or replace previously known methods for determining the identity and relatedness of individuals. The approach is generally based on alterations in nucleic acid sequences between related individuals. This analysis has been widely used in a variety of genetic, diagnostic, and forensic applications. For example, polymorphism analyses are used in identity and paternity analysis, and in genetic mapping studies.

One such type of variation is a restriction fragment length polymorphism (RFLP). RFLPS can create or delete a recognition sequence for a restriction endonuclease in one nucleic acid relative to a second nucleic acid. The result of the variation is an alteration in the relative length of restriction enzyme generated DNA fragments in the two nucleic acids.

Other polymorphisms take the form of short tandem repeats (STR) sequences, which are also referred to as variable numbers of tandem repeat (VNTR) sequences. STR sequences typically include tandem repeats of 2, 3, or 4 nucleotide sequences that are present in a nucleic acid from one individual but absent from a second, related individual at the corresponding genomic location.

Other polymorphisms take the form of single nucleotide variations, termed single nucleotide polymorphisms (SNPs), between individuals. A SNP can, in some instances, be referred to as a "cSNP" to denote that the nucleotide sequence containing the SNP originates as a cDNA.

SNPs can arise in several ways. A single nucleotide polymorphism may arise due to a substitution of one nucleotide for another at the polymorphic site. Substitutions can be transitions or transversions. A transition is the replacement of one purine nucleotide by another purine nucleotide, or one pyrimidine by another pyrimidine. A transversion is the replacement of a purine by a pyrimidine, or the converse.

Single nucleotide polymorphisms can also arise from a deletion of a nucleotide or an insertion of a nucleotide relative to a reference allele. Thus, the polymorphic site is a site at which one allele bears a gap with respect to a single nucleotide in another allele. Some SNPs

occur within, or near genes. One such class includes SNPs falling within regions of genes encoding for a polypeptide product. These SNPs may result in an alteration of the amino acid sequence of the polypeptide product and give rise to the expression of a defective or other variant protein. Such variant products can, in some cases result in a pathological condition, *e.g.*, genetic disease. Examples of genes in which a polymorphism within a coding sequence gives rise to genetic disease include sickle cell anemia and cystic fibrosis. Other SNPs do not result in alteration of the polypeptide product. Of course, SNPs can also occur in noncoding regions of genes.

SNPs tend to occur with great frequency and are spaced uniformly throughout the genome. The frequency and uniformity of SNPs means that there is a greater probability that such a polymorphism will be found in close proximity to a genetic locus of interest.

SUMMARY OF THE INVENTION

The invention is based in part on the discovery of novel single nucleotide polymorphisms (SNPs) in regions of human DNA.

Accordingly, in one aspect, the invention provides an isolated polynucleotide which includes one or more of the SNPs described herein. The polynucleotide can be, *e.g.*, a nucleotide sequence which includes one or more of the polymorphic sequences shown in Table 1 and the Sequence Listing (SEQ ID NOS: 1 - 7867) and which includes a polymorphic sequence, or a fragment of the polymorphic sequence, as long as it includes the polymorphic site. The polynucleotide may alternatively contain a nucleotide sequence which includes a sequence complementary to one or more of the sequences (SEQ ID NOS: 1-7867), or a fragment of the complementary nucleotide sequence, provided that the fragment includes a polymorphic site in the polymorphic sequence.

The polynucleotide can be, *e.g.*, DNA or RNA, and can be between about 10 and about 100 nucleotides, *e.g.* 10-90, 10-75, 10-51, 10-40, or 10-30, nucleotides in length.

In some embodiments, the polymorphic site in the polymorphic sequence includes a nucleotide other than the nucleotide listed in Table 1, column 5 for the polymorphic sequence, *e.g.*, the polymorphic site includes the nucleotide listed in Table 1, column 6 for the polymorphic sequence.

In other embodiments, the complement of the polymorphic site includes a nucleotide other than the complement of the nucleotide listed in Table 1, column 5 for the complement of the polymorphic sequence, *e.g.*, the complement of the nucleotide listed in Table 1, column 6 for the polymorphic sequence.

In some embodiments, the polymorphic sequence is associated with a polypeptide related to one of the protein families disclosed herein. For example, the nucleic acid may be associated with a polypeptide related to an ATPase associated protein, a cadherin, or any of the other proteins identified in Table 1, column 10.

In another aspect, the invention provides an isolated allele-specific oligonucleotide that hybridizes to a first polynucleotide containing a polymorphic site. The first polynucleotide can be, *e.g.*, a nucleotide sequence comprising one or more polymorphic sequences (SEQ ID NOS:1 - 7867), provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for the polymorphic sequence. Alternatively, the first polynucleotide can be a nucleotide sequence that is a fragment of the polymorphic sequence, provided that the fragment includes a polymorphic site in the polymorphic sequence, or a complementary nucleotide sequence which includes a sequence complementary to one or more polymorphic sequences (SEQ ID NOS:1 - 7867), provided that the complementary nucleotide sequence includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5. The first polynucleotide may in addition include a nucleotide sequence that is a fragment of the complementary sequence, provided that the fragment includes a polymorphic site in the polymorphic sequence.

In some embodiments, the oligonucleotide does not hybridize under stringent conditions to a second polynucleotide. The second polynucleotide can be, *e.g.*, (a) a nucleotide sequence comprising one or more polymorphic sequences (SEQ ID NOS:1 - 7867), wherein the polymorphic sequence includes the nucleotide listed in Table 1, column 5 for the polymorphic sequence; (b) a nucleotide sequence that is a fragment of any of the polymorphic sequences; (c) a complementary nucleotide sequence including a sequence complementary to one or more polymorphic sequences (SEQ ID NOS:1 - 7867), wherein the polymorphic sequence includes the complement of the nucleotide listed in Table 1, column 5; and (d) a nucleotide sequence that is a fragment of the complementary sequence, provided that the fragment includes a polymorphic site in the polymorphic sequence.

The oligonucleotide can be, *e.g.*, between about 10 and about 100 bases in length. In some embodiments, the oligonucleotide is between about 10 and 75 bases, 10 and 51 bases, 10 and about 40 bases, or about 15 and 30 bases in length.

The invention also provides a method of detecting a polymorphic site in a nucleic acid. The method includes contacting the nucleic acid with an oligonucleotide that hybridizes to a polymorphic sequence selected from the group consisting of SEQ ID NOS: 1-7867, or its complement, provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for the polymorphic sequence, or the complement includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5. The method also includes determining whether the nucleic acid and the oligonucleotide hybridize. Hybridization of the oligonucleotide to the nucleic acid sequence indicates the presence of the polymorphic site in the nucleic acid.

In preferred embodiments, the oligonucleotide does not hybridize to the polymorphic sequence when the polymorphic sequence includes the nucleotide recited in Table 1, column 5 for the polymorphic sequence, or when the complement of the polymorphic sequence includes the complement of the nucleotide recited in Table 1, column 5 for the polymorphic sequence.

The oligonucleotide can be, *e.g.*, between about 10 and about 100 bases in length. In some embodiments, the oligonucleotide is between about 10 and 75 bases, 10 and 51 bases, 10 and about 40 bases, or about 15 and 30 bases in length.

In some embodiments, the polymorphic sequence identified by the oligonucleotide is associated with a polypeptide related to one of the protein families disclosed herein. For example, the nucleic acid may be associated polypeptide related to an ATPase associated protein, cadherin, or any of the other protein families identified in Table 1, column 10.

In another aspect, the method includes determining if a sequence polymorphism is present in a subject, such as a human. The method includes providing a nucleic acid from the subject and contacting the nucleic acid with an oligonucleotide that hybridizes to a polymorphic sequence selected from the group consisting of SEQ ID NOS: 1-7867, or its complement, provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for said polymorphic sequence, or the complement includes a nucleotide other than the complement of the nucleotide recited in Table 1,

column 5. Hybridization between the nucleic acid and the oligonucleotide is then determined. Hybridization of the oligonucleotide to the nucleic acid sequence indicates the presence of the polymorphism in said subject.

In a further aspect, the invention provides a method of determining the relatedness of a first and second nucleic acid. The method includes providing a first nucleic acid and a second nucleic acid and contacting the first nucleic acid and the second nucleic acid with an oligonucleotide that hybridizes to a polymorphic sequence selected from the group consisting of SEQ ID NOS: 1-7867, or its complement, provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for the polymorphic sequence, or the complement includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5. The method also includes determining whether the first nucleic acid and the second nucleic acid hybridize to the oligonucleotide, and comparing hybridization of the first and second nucleic acids to the oligonucleotide. Hybridization of first and second nucleic acids to the nucleic acid indicates the first and second subjects are related.

In preferred embodiments, the oligonucleotide does not hybridize to the polymorphic sequence when the polymorphic sequence includes the nucleotide recited in Table 1, column 5 for the polymorphic sequence, or when the complement of the polymorphic sequence includes the complement of the nucleotide recited in Table 1, column 5 for the polymorphic sequence.

The oligonucleotide can be, *e.g.*, between about 10 and about 100 bases in length. In some embodiments, the oligonucleotide is between about 10 and 75 bases, 10 and 51 bases, 10 and about 40 bases, or about 15 and 30 bases in length.

The method can be used in a variety of applications. For example, the first nucleic acid may be isolated from physical evidence gathered at a crime scene, and the second nucleic acid may be obtained from a person suspected of having committed the crime. Matching the two nucleic acids using the method can establish whether the physical evidence originated from the person.

In another example, the first sample may be from a human male suspected of being the father of a child and the second sample may be from the child. Establishing a match using the described method can establish whether the male is the father of the child.

In another aspect, the invention provides an isolated polypeptide comprising a polymorphic site at one or more amino acid residues, and wherein the protein is encoded by a polynucleotide including one of the polymorphic sequences SEQ ID NOS:1-7867, or their complement, provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for the polymorphic sequence, or the complement includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5.

The polypeptide can be, *e.g.*, related to one of the protein families disclosed herein. For example, the polypeptide can be related to an ATPase associated protein, cadherin, or any of the other proteins provided in Table 1, column 10.

In some embodiments, the polypeptide is translated in the same open reading frame as is a wild type protein whose amino acid sequence is identical to the amino acid sequence of the polymorphic protein except at the site of the polymorphism.

In some embodiments, the polypeptide encoded by the polymorphic sequence, or its complement, includes the nucleotide listed in Table 1, column 6 for the polymorphic sequence, or the complement includes the complement of the nucleotide listed in Table 1, column 6.

The invention also provides an antibody that binds specifically to a polypeptide encoded by a polynucleotide comprising a nucleotide sequence encoded by a polynucleotide selected from the group consisting of polymorphic sequences SEQ ID NOS:1-7867, or its complement. The polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for the polymorphic sequence, or the complement includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5.

In some embodiments, the antibody binds specifically to a polypeptide encoded by a polymorphic sequence which includes the nucleotide listed in Table 1, column 6 for the polymorphic sequence.

Preferably, the antibody does not bind specifically to a polypeptide encoded by a polymorphic sequence which includes the nucleotide listed in Table 1, column 5 for the polymorphic sequence.

The invention further provides a method of detecting the presence of a polypeptide having one or more amino acid residue polymorphisms in a subject. The method includes providing a protein sample from the subject and contacting the sample with the above-described antibody under conditions that allow for the formation of antibody-antigen complexes. The antibody-antigen complexes are then detected. The presence of the complexes indicates the presence of the polypeptide.

The invention also provides a method of treating a subject suffering from, at risk for, or suspected of, suffering from a pathology ascribed to the presence of a sequence polymorphism in a subject, *e.g.*, a human, non-human primate, cat, dog, rat, mouse, cow, pig, goat, or rabbit. The method includes providing a subject suffering from a pathology associated with aberrant expression of a first nucleic acid comprising a polymorphic sequence selected from the group consisting of SEQ ID NOS:1 - 7867, or its complement, and treating the subject by administering to the subject an effective dose of a therapeutic agent. Aberrant expression can include qualitative alterations in expression of a gene, *e.g.*, expression of a gene encoding a polypeptide having an altered amino acid sequence with respect to its wild-type counterpart. Qualitatively different polypeptides can include, shorter, longer, or altered polypeptides relative to the amino acid sequence of the wild-type polypeptide. Aberrant expression can also include quantitative alterations in expression of a gene. Examples of quantitative alterations in gene expression include lower or higher levels of expression of the gene relative to its wild-type counterpart, or alterations in the temporal or tissue-specific expression pattern of a gene. Finally, aberrant expression may also include a combination of qualitative and quantitative alterations in gene expression.

The therapeutic agent can be administered to a subject suffering from a pathology associated with aberrant expression of a first nucleic acid comprising a polymorphic sequence. The therapeutic agent can include, e.g., second nucleic acid comprising the polymorphic sequence, provided that the second nucleic acid comprises the nucleotide present in the wild type allele. In some embodiments, the second nucleic acid sequence comprises a polymorphic sequence which includes the nucleotide listed in Table 1, column 5 for the polymorphic sequence.

Alternatively, the therapeutic agent can be a polypeptide encoded by a polynucleotide comprising a polymorphic sequence selected from the group consisting of SEQ ID NOS:1 - 7867, or by a polynucleotide comprising a nucleotide sequence that is complementary to any

one of the polymorphic sequences SEQ ID NOS:1 - 7867, provided that the polymorphic sequence includes the nucleotide listed in Table 1, column 6 for the polymorphic sequence.

The therapeutic agent may further include an antibody as herein described, or an oligonucleotide comprising a polymorphic sequence selected from the group consisting of SEQ ID NOS:1 - 7867, or by a polynucleotide comprising a nucleotide sequence that is complementary to any one of polymorphic sequences SEQ ID NOS:1 - 7867, provided that the polymorphic sequence includes the nucleotide listed in Table 1, column 5 or Table 1, column 6 for the polymorphic sequence.

In another aspect, the invention provides an oligonucleotide array comprising one or more oligonucleotides hybridizing to a first polynucleotide at a polymorphic site encompassed therein. The first polynucleotide can be, e.g., a nucleotide sequence comprising one or more polymorphic sequences (SEQ ID NOS:1 - 7867); a nucleotide sequence that is a fragment of any of the nucleotide sequences, provided that the fragment includes a polymorphic site in the polymorphic sequence; a complementary nucleotide sequence comprising a sequence complementary to one or more polymorphic sequences (SEQ ID NOS:1 - 7867); or a nucleotide sequence that is a fragment of the complementary sequence, provided that the fragment includes a polymorphic site in the polymorphic sequence.

In preferred embodiments, the array comprises 10; 100; 1,000; 10,000; 100,000 or more oligonucleotides.

The invention also provides a kit comprising one or more of the herein-described nucleic acids. The kit can include, e.g., a polynucleotide which includes one or more of the SNPs described herein. The polynucleotide can be, e.g., a nucleotide sequence which includes one or more of the polymorphic sequences shown in Table 1 and the Sequence Listing (SEQ ID NOS: 1 - 7867) and which includes a polymorphic sequence, or a fragment of the polymorphic sequence, as long as it includes the polymorphic site. The polynucleotide may alternatively contain a nucleotide sequence which includes a sequence complementary to one or more of the sequences (SEQ ID NOS:1-7867), or a fragment of the complementary nucleotide sequence, provided that the fragment includes a polymorphic site in the polymorphic sequence. The invention provides an isolated allele-specific oligonucleotide that hybridizes to a first polynucleotide containing a polymorphic site. The first polynucleotide can be, e.g., a nucleotide sequence comprising one or more polymorphic

sequences (SEQ ID NOS:1 - 7867), provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for the polymorphic sequence. Alternatively, the first polynucleotide can be a nucleotide sequence that is a fragment of the polymorphic sequence, provided that the fragment includes a polymorphic site in the polymorphic sequence, or a complementary nucleotide sequence which includes a sequence complementary to one or more polymorphic sequences (SEQ ID NOS:1 - 7867), provided that the complementary nucleotide sequence includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5. The first polynucleotide may in addition include a nucleotide sequence that is a fragment of the complementary sequence, provided that the fragment includes a polymorphic site in the polymorphic sequence.

Unless otherwise defined, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Although methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present invention, suitable methods and materials are described below. All publications, patent applications, patents, and other references mentioned herein are incorporated by reference in their entirety. In the case of conflict, the present specification, including definitions, will control. In addition, the materials, methods, and examples are illustrative only and not intended to be limiting.

Other features and advantages of the invention will be apparent from the following detailed description and claims.

DETAILED DESCRIPTION OF THE INVENTION

The invention provides human SNPs in sequences which are transcribed, *i.e.*, are cSNPs. Many SNPs have been identified in genes related to polypeptides of known function. If desired, SNPs associated with various polypeptides can be used together. For example, SNPs can be grouped according to whether they are derived from a nucleic acid encoding a polypeptide related to particular protein family or involved in a particular function. Similarly, SNPs can be grouped according to the functions played by their gene products. Such functions include, structural proteins, proteins which are associated with metabolic pathways, including fatty acid metabolism, glycolysis, intermediary metabolism, calcium metabolism, proteases, and amino acid metabolism, etc. Specifically, the present invention

provides a large number of human cSNP's based on at least one gene product that has not been previously identified. In contrast, and as defined specifically in the following paragraph, the cSNP's involve nucleic acid sequences that are assembled from at least one known sequence.

The present invention provides a large number of human cSNP's based on at least one gene product that has not been previously identified. In contrast, and as defined specifically in the following paragraph, the cSNP's involve nucleic acid sequences that are assembled from at least one known sequence.

7867 distinct polymorphic sites were identified by the present inventors, using the following procedure. Raw traces underlying sequence data were drawn from public databases and from the proprietary database of the Assignee of the present invention. The sequences were obtained by calling the bases from these traces, and included assigning "Phred" quality scores for each called base. For each allelic set, at the polynucleotide level, four or more nucleotide sequences were identified having at least partial overlap with one another.

As illustrated in FIG. 1, these four or more sequences could be clustered and assembled to make a consensus contig that included an ORF. In this way, the inventors found that the assembled contigs defined associated sets of two, or possibly more than two, alleles defined by an SNP at a particular polymorphic site. In order to be confirmed as a SNP site, the nucleotide change from the consensus sequence had to occur in at least two individual sequences, and had to have a "Phred" score of 23 or higher at the site of the presumed SNP. Furthermore, in a window of 5 bases on either side of the SNP, no more than 50% mismatching with the consensus sequence was allowed. In the assembly leading to each of the contigs defining the allelic set, the SNP alleles occur in polynucleotides found in public databases. Furthermore, it was found that the assembled contigs defined associated sets of two, or possibly more than two, alleles defined by an SNP at a particular polymorphic site. These associations were not previously known. The SNPs are presented in Table 1.

At the level of translation of an ORF contained in the contigs, however, the inventors identified allelic sets in which one allele defines a known polypeptide sequence that includes the polymorphic site and another polypeptide allele is not previously known. Then, various associations of alleles are possible. For example, it is possible that an allelic pair is defined

in a noncoding region of the contig containing an ORF. In such cases the inventors believe that the invention resides in the recognition of the allelic pair; this association has not heretofore been made. Alternatively, sets of allelic contigs may exist in which the polymorphic site is within an ORF, but does not result in an amino acid change among the allelic polypeptides. Here too it is believed that the invention resides in the recognition of the allelic pair; and that this association has not heretofore been made. In yet another alternative, the polymorphic site resides within an ORF and results in an amino acid change, or a frameshift, among the alleles of the allelic set. In the sets of gene products that fall within this group, at least one of the alleles at the polypeptide level is a known protein. At least one of the remaining allele or alleles in the set, carrying a variant amino acid at the polymorphic site, is a novel polypeptide not heretofore known. The invention resides at least in the recognition of the polymorphic allele as being a variant of the known reference polypeptide.

Table 1 provides information concerning the allelic sequences. One of the sequences may be termed a reference polymorphic sequence, and the corresponding second sequence includes the variant SNP at the polymorphic site. Since the reference polypeptide sequence is already known, the Sequence Listing accompanying this application provides only the sequence of the polymorphic allele, while its SEQ ID NO is provided in the Table. A reference to the SEQ ID NO that corresponds to the translated amino acid sequence is also given. The Table includes thirteen columns that provide descriptive information for each cSNP, each of which occupies one row in the Table. The column headings, and a description of each, are given below.

SNPs disclosed in Table 1 were detected by aligning large numbers of sequences from genetically diverse sources of publicly available mRNA libraries (Clontech). Software designed specifically to look for multiple examples of variant bases differing from a consensus sequence was created and deployed. A criteria of a minimum of 2 occurrences of a sequence differing from the consensus in high quality sequence reads was used to identify an SNP.

The SNPs described herein may be useful in diagnostic kits, for DNA arrays on chips and for other uses that involve hybridization of the SNP.

Specific SNPs may have utility where a disease has already been associated with that gene. Examples of possible disease correlations between the claimed SNPs with members of the genes of each classification are listed below:

Amylases

Amylase is responsible for endohydrolysis of 1,4-alpha-glucosidic linkages in oligosaccharides and polysaccharides. Variations in amylase gene may be indicative of delayed maturation and of various amylase producing neoplasms and carcinomas.

Amyloid

The serum amyloid A (SAA) proteins comprise a family of vertebrate proteins that associate predominantly with high density lipoproteins (HDL). The synthesis of certain members of the family is greatly increased in inflammation. Prolonged elevation of plasma SAA levels, as in chronic inflammation, 15 results in a pathological condition, called amyloidosis, which affectsthe liver, kidney and spleen and which is characterized by the highly insoluble accumulation of SAA in these tissues. Amyloid selectively inhibits insulin-stimulated glucose utilization and glycogen deposition in muscle, while not affecting adipocyte glucose metabolism. Deposition of fibrillar amyloid proteins intraneuronally, as neurofibrillary tangles, extracellularly, as plaques and in blood vessels, is characteristic of both Alzheimer's disease and aged Down's syndrome. Amyloid deposition is also associated with type II diabetes mellitus.

Angiopoeitin

Members of the angiopoeitin/fibrinogen family have been shown to stimulate the generation of new blood vessels, inhibit the generation of new blood vessels, and perform several roles in blood clotting. This generation of new blood vessels, called angiogenesis, is also an essential step in tumor growth in order for the tumor to get the blood supply it needs to expand. Variation in these genes may be predictive of any form of heart disease, numerous blood clotting disorders, stroke, hypertension and predisposition to tumor formation and metastasis. In particular, these variants may be predictive of the response to various antihypertensive drugs and chemotherapeutic and anti-tumor agents.

Apoptosis-related proteins

Active cell suicide (apoptosis) is induced by events such as growth factor withdrawal and toxins. It is controlled by regulators, which have either an inhibitory effect on programmed cell death (anti-apoptotic) or block the protective effect of inhibitors (pro-apoptotic). Many viruses have found a way of countering defensive apoptosis by encoding their own anti-apoptosis genes preventing their target-cells from dying too soon. Variants of apoptosis related genes may be useful in formulation of antiaging drugs.

Cadherin, Cyclin, Polymerase, Oncogenes, Histones, Kinases

Members of the cell division/cell cycle pathways such as cyclins, many transcription factors and kinases, DNA polymerases, histones, helicases and other oncogenes play a critical role in carcinogenesis where the uncontrolled proliferation of cells leads to tumor formation and eventually metastasis. Variation in these genes may be predictive of predisposition to any form of cancer, from increased risk of tumor formation to increased rate of metastasis. In particular, these variants may be predictive of the response to various chemotherapeutic and anti-tumor agents.

Colony-stimulating factor-related proteins

Granulocyte/macrophage colony-stimulating factors are cytokines that act in hematopoiesis by controlling the production, differentiation, and function of 2 related white cell populations of the blood, the granulocytes and the monocytes-macrophages.

Complement-related proteins

Complement proteins are immune associated cytotoxic agents, acting in a chain reaction to exterminate target cells to that were opsonized (primed) with antibodies, by forming a membrane attack complex (MAC). The mechanism of killing is by opening pores in the target cell membrane. Variations in 20 complement genes or their inhibitors are associated with many autoimmune disorders. Modified serum levels of complement products cause edemas of various tissues, lupus (SLE), vasculitis, glomerulonephritis, renal failure, hemolytic anemia, thrombocytopenia, and arthritis. They interfere with mechanisms of ADCC (antibody dependent cell cytotoxicity), severely impair immune competence and reduce phagocytic ability. Variants of complement genes may also be indicative of type I

diabetes mellitus, meningitis neurological disorders such as Nemaline myopathy, Neonatal hypotonia, muscular disorders such as congenital myopathy and other diseases.

Cytochrome

The respiratory chain is a key biochemical pathway which is essential to all aerobic cells. There are five different cytochromes involved in the chain. These are heme bound proteins which serve as electron carriers. Modifications in these genes may be predictive of ataxia areflexia, dementia and myopathic and neuropathic changes in muscles. Also, association with various types of solid tumors.

Kinesins

Kinesins are tubulin molecular motors that function to transport organelles within cells and to move chromosomes along microtubules during cell division. Modifications of these genes may be indicative of neurological disorders such as Pick disease of the brain, tuberous sclerosis.

Cytokines, Interferon, Interleukin

Members of the cytokine families are known for their potent ability to stimulate cell growth and division even at low concentrations. Cytokines such as erythropoietin are cell-specific in their growth stimulation; erythropoietin is useful for the stimulation of the proliferation of erythroblasts. Variants in cytokines may be predictive for a wide variety of diseases, including cancer predisposition.

G-protein coupled receptors

G-protein coupled receptors (also called R7G) are an extensive group of hormones, neurotransmitters, odorants and light receptors which transduce extracellular signals by interaction with guanine nucleotide-binding (G) proteins. Alterations in genes coding for G-coupled proteins may be involved in and indicative of a vast number of physiological conditions. These include blood pressure regulation, renal dysfunctions, male infertility, dopamine associated cognitive, emotional, and endocrine functions, hypercalcemia, chondrodysplasia and osteoporosis, pseudohypoparathyroidism, growth retardation and dwarfism.

Thioesterases

Eukaryotic thiol proteases are a family of proteolytic enzymes which contain an active site cysteine. Catalysis proceeds through a thioester intermediate and is facilitated by a nearby histidine side chain; an asparagine completes the essential catalytic triad. Variants of thioester associated genes may be predictive of neuronal disorders and mental illnesses such as Ceroid Lipoffiscinosis, Neuronal 1, Infantile, Santavuori disease and more.

The SNPs are shown in Table 1 and the Sequence Listing. Both provide a summary of the polymorphic sequences disclosed herein. In the Table, a "SNP" is a polymorphic site embedded in a polymorphic sequence. The polymorphic site is occupied by a single nucleotide, which is the position of nucleotide variation between the wild type and polymorphic allelic sequences. The site is usually preceded by and followed by relatively highly conserved sequences of the allele (e.g., sequences that vary in less than 1/100 or 1/1000 members of the populations). Thus, a polymorphic sequence can include one or more of the following sequences: (1) a sequence having the nucleotide denoted in Table 1, column 5 at the polymorphic site in the polymorphic sequence; or (2) a sequence having a nucleotide other than the nucleotide denoted in Table 1, column 5 at the polymorphic site in the polymorphic sequence. An example of the latter sequence is a polymorphic sequence having the nucleotide denoted in Table 1, column 6 at the polymorphic site in the polymorphic sequence.

Nucleotide sequences for a referenced-polymorphic pair are presented in Table 1. Each cSNP entry provides information concerning the wild type nucleotide sequence as well as the corresponding sequence that includes the SNP at the polymorphic site. Since the wild type sequence is already known, the Sequence Listing accompanying this application provides only the sequence of the polymorphic allele; its SEQ ID NO: is also cross referenced in the Table 1. A reference to the SEQ ID NO: giving the translated amino acid sequence is also given if appropriate. The Table includes thirteen columns that provide descriptive information for each cSNP, each of which occupies one row in the Table. The column headings, and an explanation for each, are given below.

"SEQ ID" provides the cross-references to the nucleotide SEQ ID NOs: for the polymorphic sequences, which are numbered consecutively, and, as explained below, amino acid SEQ ID NOs: as well, in the Sequence Listing of the application. Conversely, each

sequence entry in the Sequence Listing also includes a cross-reference to the CuraGen sequence ID, under the label "CuraGen sequence ID". The first SEQ ID NO: given in the first column of each row of the Table is the SEQ ID NO: identifying the nucleic acid sequence for the polymorphisms. If a polymorphism carries an entry for an amino acid in a coding region, then a second SEQ ID NO: appears in parentheses in the column "Amino acid after" (see below) for the polymorphic amino acid sequence . The latter SEQ ID NOs: refer to amino acid sequences giving the polymorphic amino acid sequences that are the translation of the nucleotide polymorphism. If a polymorphism carries no entry for the protein portion of the row, only one SEQ ID NO: is provided, in the first column.

"Base pos. of SNP" gives the numerical position of the nucleotide in the nucleic acid at which the cSNP is found, as identified in this invention.

"Polymorphic sequence" provides a 51-base sequence with the polymorphic site at the 26th base in the sequence, as well as 25 bases from the reference sequence on the 5' side and the 3' side of the polymorphic site. The designation at the polymorphic site is enclosed in square brackets, and provides first, the reference nucleotide; second, a "slash (/)"; and third, the polymorphic nucleotide. In certain cases the polymorphism is an insertion or a deletion. In that case, the position which is "unfilled" (i.e., the reference or the polymorphic position) is indicated by the word "gap".

"Base before" provides the nucleotide present in the reference sequence at the position at which the polymorphism is found.

"Base after" provides the altered nucleotide at the position of the polymorphism.

"Amino acid before" provides the amino acid in the reference protein, if the polymorphism occurs in a coding region.

"Amino acid after" provides the amino acid in the polymorphic protein, if the polymorphism occurs in a coding region. This column also includes the SEQ ID NO: in parentheses for the translated polymorphic amino acid sequence if the polymorphism occurs in a coding region.

"Type of change" provides information on the nature of the polymorphism.

"SILENT-NONCODING" is used if the polymorphism occurs in a noncoding region of a nucleic acid.

"SILENT-CODING" is used if the polymorphism occurs in a coding region of a nucleic acid of a nucleic acid and results in no change of amino acid in the translated polymorphic protein.

"CONSERVATIVE" is used if the polymorphism occurs in a coding region of a nucleic acid and provides a change in which the altered amino acid falls in the same class as the reference amino acid. The classes are:

Aliphatic: Gly, Ala, Val, Leu, Ile;

Aromatic: Phe, Tyr, Trp;

Sulfur-containing: Cys, Met;

Aliphatic OH: Ser, Thr;

Basic: Lys, Arg, His;

Acidic: Asp, Glu, Asn, Gln;

Pro falls in none of the other classes; and

End defines a termination codon.

"NONCONSERVATIVE" is used if the polymorphism occurs in a coding region of a nucleic acid and provides a change in which the altered amino acid falls in a different class than the reference amino acid.

"FRAMESHIFT" relates to an insertion or a deletion. If the frameshift occurs in a coding region, the Table provides the translation of the frameshifted codons 3' to the polymorphic site.

"Protein classification of CuraGen gene" provides a generic class into which the protein is classified. During the course of the work leading to the filing of the four applications identified above, approximately 100 classes of proteins were identified.

"Name of protein identified following a BLASTX analysis of the CuraGen sequence" provides the database reference for the protein found to resemble the novel reference-polymorphism cognate pair most closely. (The next paragraph explains how a sequence was determined to be "novel").

"Similarity (pvalue) following a BLASTX analysis" provides the pvalue, a statistical measure from the BLASTX analysis that the polymorphic sequence is similar to, and therefore an allele of, the reference, or wild-type, sequence. In the present application, a cutoff of pvalue > 1×10^{-50} (entered, for example, as 1.0E-50 in the Table) is used to establish that the reference-polymorphic cognate pairs are novel.

"Map location" provides any information available at the time of filing related to localization of a gene on a chromosome.

The polymorphisms are arranged in the Table in the following order.

SEQ ID NOs: 1-5696 are nucleotide sequences for SNPs that are silent.

SEQ ID NOs: 5697-6011 are nucleotide sequences for SNPs that lead to conservative amino acid changes.

SEQ ID NOs: 6012-6740 are nucleotide sequences for SNPs that lead to nonconservative amino acid changes.

SEQ ID NOs: 6741-7867 are nucleotide sequences for SNPs that involve a gap. With respect to the reference or wild-type sequence at the position of the polymorphism, the allelic cSNP introduces an additional nucleotide (an insertion) or deletes a nucleotide (a deletion). An SNP that involves a gap generates a frame shift.

SEQ ID NOs: 7868-8182 are the amino acid sequences centered at the polymorphic amino acid residue for the protein products provided by SNPs that lead to conservative amino acid changes. 7 or 8 amino acids on either side of the polymorphic site are shown. The order in which these sequences appear mirrors the order of presentation of the cognate nucleotide sequences, and is set forth in the Table.

SEQ ID NOs: 8183-8911 are the amino acid sequences centered at the polymorphic amino acid residue for the protein products provided by SNPs that lead to nonconservative

amino acid changes. 7 or 8 amino acids on either side of the polymorphic site are shown. The order in which these sequences appear mirrors the order of presentation of the cognate nucleotide sequences, and is set forth in the Table.

SEQ ID NOs: 8912-10038 are the amino acid sequences centered at the polymorphic amino acid residue for the protein products provided by SNPs that lead to frameshift-induced amino acid changes. 7 or 8 amino acids on either side of the polymorphic site are shown. The order in which these sequences appear mirrors the order of presentation of the cognate nucleotide sequences, and is set forth in the Table.

Provided herein are compositions which include, or are capable of detecting, nucleic acid sequences having these polymorphisms, as well as methods of using nucleic acids.

IDENTIFICATION OF INDIVIDUALS CARRYING SNPS

Individuals carrying polymorphic alleles of the invention may be detected at either the DNA, the RNA, or the protein level using a variety of techniques that are well known in the art. Strategies for identification and detection are described in *e.g.*, EP 730,663, EP 717,113, and PCT US97/02102. The present methods usually employ pre-characterized polymorphisms. That is, the genotyping location and nature of polymorphic forms present at a site have already been determined. The availability of this information allows sets of probes to be designed for specific identification of the known polymorphic forms.

Many of the methods described below require amplification of DNA from target samples. This can be accomplished by e.g., PCR. See generally PCR Technology: Principles and Applications for DNA Amplification (ed. H.A. Erlich, Freeman Press, NY, NY, 1992); PCR Protocols: A Guide to Methods and Applications (eds. Innis, et al., Academic Press, San Diego, CA, 1990); Mattila et al., Nucleic Acids Res. 19, 4967 (1991); Eckert et al., PCR Methods and Applications 1, 17 (1991); PCR (eds. McPherson et al., IRL Press, Oxford); and U.S. Patent 4,683,202.

The phrase "recombinant protein" or "recombinantly produced protein" refers to a peptide or protein produced using non-native cells that do not have an endogenous copy of DNA able to express the protein. In particular, as used herein, a recombinantly produced protein relates to the gene product of a polymorphic allele, i.e., a "polymorphic protein"

containing an altered amino acid at the site of translation of the nucleotide polymorphism. The cells produce the protein because they have been genetically altered by the introduction of the appropriate nucleic acid sequence. The recombinant protein will not be found in association with proteins and other subcellular components normally associated with the cells producing the protein. The terms "protein" and "polypeptide" are used interchangeably herein.

The phrase "substantially purified" or "isolated" when referring to a nucleic acid, peptide or protein, means that the chemical composition is in a milieu containing fewer, or preferably, essentially none, of other cellular components with which it is naturally associated. Thus, the phrase "isolated" or "substantially pure" refers to nucleic acid preparations that lack at least one protein or nucleic acid normally associated with the nucleic acid in a host cell. It is preferably in a homogeneous state although it can be in either a dry or aqueous solution. Purity and homogeneity are typically determined using analytical chemistry techniques such as gel electrophoresis or high performance liquid chromatography. Generally, a substantially purified or isolated nucleic acid or protein will comprise more than 80% of all macromolecular species present in the preparation. Preferably, the nucleic acid or protein is purified to represent greater than 90% of all macromolecular species present. More preferably the nucleic acid or protein is purified to greater than 95%, and most preferably the nucleic acid or protein is purified to essential homogeneity, wherein other macromolecular species are not detected by conventional analytical procedures.

The genomic DNA used for the diagnosis may be obtained from any nucleated cells of the body, such as those present in peripheral blood, urine, saliva, buccal samples, surgical specimen, and autopsy specimens. The DNA may be used directly or may be amplified enzymatically in vitro through use of PCR (Saiki et al. Science 239:487-491 (1988)) or other in vitro amplification methods such as the ligase chain reaction (LCR) (Wu and Wallace Genomics 4:560-569 (1989)), strand displacement amplification (SDA) (Walker et al. Proc. Natl. Acad. Sci. U.S.A. 89:392-396 (1992)), self-sustained sequence replication (3SR) (Fahy et al. PCR Methods P&J& 1:25-33 (1992)), prior to mutation analysis.

The method for preparing nucleic acids in a form that is suitable for mutation detection is well known in the art. A "nucleic acid" is a deoxyribonucleotide or ribonucleotide polymer in either single-or double-stranded form, including known analogs of natural nucleotides unless otherwise indicated. The term "nucleic acids", as used herein,

refers to either DNA or RNA. "Nucleic acid sequence" or "polynucleotide sequence" refers to a single-stranded sequence of deoxyribonucleotide or ribonucleotide bases read from the 5' end to the 3' end. The direction of 5' to 3' addition of nascent RNA transcripts is referred to as the transcription direction; sequence regions on the DNA strand having the same sequence as the RNA and which are beyond the 5' end of the RNA transcript in the 5' direction are referred to as "upstream sequences"; sequence regions on the DNA strand having the same sequence as the RNA and which are beyond the 3' end of the RNA transcript in the 3' direction are referred to as "downstream sequences". The term includes both self-replicating plasmids, infectious polymers of DNA or RNA and nonfunctional DNA or RNA. The complement of any nucleic acid sequence of the invention is understood to be included in the definition of that sequence. "Nucleic acid probes" may be DNA or RNA fragments.

The detection of polymorphisms in specific DNA sequences, can be accomplished by a variety of methods including, but not limited to, restriction-fragment-length-polymorphism detection based on allele-specific restriction-endonuclease cleavage (Kan and Dozy Lancet ii:910-912 (1978)), hybridization with allele-specific oligonucleotide probes (Wallace et al. Nucl. Acids Res. 6:3543-3557 (1978)), including immobilized oligonucleotides (Saiki et al. Proc. Natl. Acad. SCI. USA, 86:6230-6234 (1969)) or oligonucleotide arrays (Maskos and Southern Nucl. Acids Res 21:2269-2270 (1993)), allele-specific PCR (Newton et al. Nucl Acids Res 17:2503-2516 (1989)), mismatch-repair detection (MRD) (Faham and Cox Genome Res 5:474-482 (1995)), binding of MutS protein (Wagner et al. Nucl Acids Res 23:3944-3948 (1995), denaturing-gradient gel electrophoresis (DGGE) (Fisher and Lerman et al. *Proc. Natl. Acad. Sci. U.S.A. 80:1579-l* 583 (1983)), single-strand-conformation-polymorphism detection (Orita et al. Genomics 5:874-879 (1983)), RNAase cleavage at mismatched base-pairs (Myers et al. Science 230:1242 (1985)), chemical (Cotton et al. Proc. Natl. w Sci. U.S.A, 8Z4397-4401 (1988)) or enzymatic (Youil et al. Proc. Natl. Acad. Sci. U.S.A. 92:87-91 (1995)) cleavage of heteroduplex DNA, methods based on allele specific primer extension (Syvanen et al. Genomics 8:684-692 (1990)), genetic bit analysis (GBA) (Nikiforov et al. &&I Acids 22:4167-4175 (1994)), the oligonucleotide-ligation assay (OLA) (Landegren et al. Science 241:1077 (1988)), the allele-specific ligation chain reaction (LCR) (Barrany Proc. Natl. Acad. Sci. U.S.A. 88:189-l 93 (1991)), gap-LCR (Abravaya et al. Nucl Acids Res 23:675-682 (1995)), radioactive and/or fluorescent DNA sequencing using standard procedures well known in the art, and peptide nucleic acid (PNA) assays (Orum et al., Nucl. Acids Res, 21:5332-5356 (1993); Thiede et al., Nucl. Acids Res. 24:983-984

(1996)).

"Specific hybridization" or "selective hybridization" refers to the binding, or duplexing, of a nucleic acid molecule only to a second particular nucleotide sequence to which the nucleic acid is complementary, under suitably stringent conditions when that sequence is present in a complex mixture (e.g., total cellular DNA or RNA). "Stringent conditions" are conditions under which a probe will hybridize to its target subsequence, but to no other sequences. Stringent conditions are sequence-dependent and are different in different circumstances. Longer sequences hybridize specifically at higher temperatures than shorter ones. Generally, stringent conditions are selected such that the temperature is about 5°C lower than the thermal melting point (Tm) for the specific sequence to which hybridization is intended to occur at a defined ionic strength and pH. The Tm is the temperature (under defined ionic strength, pH, and nucleic acid concentration) at which 50% of the target sequence hybridizes to the complementary probe at equilibrium. Typically, stringent conditions include a salt concentration of at least about 0.01 to about 1.0 M Na ion concentration (or other salts), at pH 7.0 to 8.3. The temperature is at least about 30°C for short probes (e.g., 10 to 50 nucleotides) . Stringent conditions can also be achieved with the addition of destabilizing agents such as formamide. For example, conditions of 5X SSPE (750 mM NaCl, 50 mM NaPhosphate, 5 mM EDTA, pH 7.4) and a temperature of 25-30°C are suitable for allele-specific probe hybridization.

"Complementary" or "target" nucleic acid sequences refer to those nucleic acid sequences which selectively hybridize to a nucleic acid probe. Proper annealing conditions depend, for example, upon a probe's length, base composition, and the number of mismatches and their position on the probe, and must often be determined empirically. For discussions of nucleic acid probe design and annealing conditions, see, for example, Sambrook et al., or Current Protocols in Molecular Biology, F. Ausubel *et* al., ed., Greene Publishing and Wiley-Interscience, New York (1987).

A perfectly matched probe has a sequence perfectly complementary to a particular target sequence. The test probe is typically perfectly complementary to a portion of the target sequence. A "polymorphic" marker or site is the locus at which a sequence difference occurs with respect to a reference sequence. Polymorphic markers include restriction fragment length polymorphisms, variable number of tandem repeats (VNTR's), hypervariable regions, minisatellites, dinucleotide repeats, trinucleotide repeats, tetranucleotide repeats, simple

sequence repeats, and insertion elements such as Alu. The reference allelic form may be, for example, the most abundant form in a population, or the first allelic form to be identified, and other allelic forms are designated as alternative, variant or polymorphic alleles. The allelic form occurring most frequently in a selected population is sometimes referred to as the "wild type" form, and herein may also be referred to as the "reference" form. Diploid organisms may be homozygous or heterozygous for allelic forms. A diallelic polymorphism has two distinguishable forms (i.e., base sequences), and a triallelic polymorphism has three such forms.

As used herein an "oligonucleotide" is a single-stranded nucleic acid ranging in length from 2 to about 60 bases. Oligonucleotides are often synthetic but can also be produced from naturally occurring polynucleotides. A probe is an oligonucleotide capable of binding to a target nucleic acid of a complementary sequence through one or more types of chemical bonds, usually through complementary base pairing via hydrogen bond formation. Oligonucleotides probes are often between 5 and 60 bases, and, in specific embodiments, may be between 10-40, or 15-30 bases long. An oligonucleotide probe may include natural (i.e. A, G, C, or T) or modified bases (7-deazaguanosine, inosine, etc.). In addition, the bases in an oligonucleotide probe may be joined by a linkage other than a phosphodiester bond, such as a phosphoramidite linkage or a phosphorothioate linkage, or they may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than by phosphodiester bonds, so long as it does not interfere with hybridization.

As used herein, the term "primer" refers to a single-stranded oligonucleotide which acts as a point of initiation of template-directed DNA synthesis under appropriate conditions (e.g., in the presence of four different nucleoside triphosphates and a polymerization agent, such as DNA polymerase, RNA polymerase or reverse transcriptase) in an appropriate buffer and at a suitable temperature. The appropriate length of a primer depends on the intended use of the primer, but typically ranges from 15 to 30 nucleotides. Short primer molecules generally require cooler temperatures to form sufficiently stable hybrid complexes with the template. A primer need not be perfectly complementary to the exact sequence of the template, but should be sufficiently complementary to hybridize with it. The term "primer site" refers to the sequence of the target DNA to which a primer hybridizes. The term "primer pair" refers to a set of primers including a 5' (upstream) primer that hybridizes with the 5' end of the DNA sequence to be amplified and a 3' (downstream) primer that hybridizes with the complement of the 3' end of the sequence to be amplified.

DNA fragments can be prepared, for example, by digesting plasmid DNA, or by use of PCR. Oligonucleotides for use as primers or probes are chemically synthesized by methods known in the field of the chemical synthesis of polynucleotides, including by way of non-limiting example the phosphoramidite method described by Beaucage and Carruthers, Tetrahedron Lett 22:1859-l 862 (1981) and the triester method provided by Matteucci, et al., J. Am. Chem. Soc., 103:3185 (1981) both incorporated herein by reference. These syntheses may employ an automated synthesizer, as described in Needham-VanDevanter, D.R., et al., Nucleic Acids Res. 12:61596168 (1984). Purification of oligonucleotides may be carried out by either native acrylamide gel electrophoresis or by anion-exchange HPLC as described in Pearson, J.D. and Regnier, F.E., ,J. Chrom,, 255:137-149 (1983). A double stranded fragment may then be obtained, if desired, by annealing appropriate complementary single strands together under suitable conditions or by synthesizing the complementary strand using a DNA polymerase with an appropriate primer sequence. Where a specific sequence for a nucleic acid probe is given, it is understood that the complementary strand is also identified and included. The complementary strand will work equally well in situations where the target is a double-stranded nucleic acid.

The sequence of the synthetic oligonucleotide or of any nucleic acid fragment can be can be obtained using either the dideoxy chain termination method or the Maxam-Gilbert method (see Sambrook et al. Molecular Cloning - a Laboratory Manual (2nd Ed.), Vols. 1-3, Cold Spring Harbor Laboratory, Cold Spring Harbor, New York, (1989), which is incorporated herein by reference. This manual is hereinafter referred to as "Sambrook et al." ; Zyskind et al., (1988)). Recombinant DNA Laboratory Manual, (Acad. Press, New York). Oligonucleotides useful in diagnostic assays are typically at least 8 consecutive nucleotides in length, and may range upwards of 18 nucleotides in length to greater than 100 or more consecutive nucleotides.

Another aspect of the invention pertains to isolated antisense nucleic acid molecules that are hybridizable to or complementary to the nucleic acid molecule comprising the SNP-containing nucleotide sequences of the invention, or fragments, analogs or derivatives thereof. An "antisense" nucleic acid comprises a nucleotide sequence that is complementary to a "sense" nucleic acid encoding a protein, *e.g.*, complementary to the coding strand of a double-stranded cDNA molecule or complementary to an mRNA sequence. In specific

aspects, antisense nucleic acid molecules are provided that comprise a sequence complementary to at least about 10, about 25, about 50, or about 60 nucleotides or an entire SNP coding strand, or to only a portion thereof.

In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a polymorphic nucleotide sequence of the invention. The term "coding region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid. In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence of the invention. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (*i.e.*, also referred to as 5' and 3' untranslated regions).

Given the coding strand sequences disclosed herein, antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick or Hoogsteen base pairing. For example, the antisense nucleic acid molecule can generally be complementary to the entire coding region of an mRNA, but more preferably as embodied herein, it is an oligonucleotide that is antisense to only a portion of the coding or noncoding region of the mRNA. An antisense oligonucleotide can range in length between about 5 and about 60 nucleotides, preferably between about 10 and about 45 nucleotides, more preferably between about 15 and 40 nucleotides, and still more preferably between about 15 and 30 in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis or enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (*e.g.*, an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, *e.g.*, phosphorothioate derivatives and acridine substituted nucleotides can be used.

Examples of modified nucleotides that can be used to generate the antisense nucleic acid include: 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxylmethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine,

7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (*i.e.*, RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following section).

The antisense nucleic acid molecules of the invention are typically administered to a subject or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding a polymorphic protein to thereby inhibit expression of the protein, *e.g.*, by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementary to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule that binds to DNA duplexes, through specific interactions in the major groove of the double helix. An example of a route of administration of antisense nucleic acid molecules of the invention includes direct injection at a tissue site. Alternatively, antisense nucleic acid molecules can be modified to target selected cells and then administered systemically. For example, for systemic administration, antisense molecules can be modified such that they specifically bind to receptors or antigens expressed on a selected cell surface, *e.g.*, by linking the antisense nucleic acid molecules to peptides or antibodies that bind to cell surface receptors or antigens. The antisense nucleic acid molecules can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong pol II or pol III promoter are preferred.

In yet another embodiment, the antisense nucleic acid molecule of the invention is an α-anomeric nucleic acid molecule. An α-anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual -units, the strands run parallel to each other (Gaultier *et al.* (1987) *Nucleic Acids Res* 15: 6625-6641). The antisense nucleic acid molecule can also comprise a 2'-o-methylribonucleotide (Inoue *et*

al. (1987) *Nucleic Acids Res* 15: 6131-6148) or a chimeric RNA -DNA analogue (Inoue *et al.* (1987) *FEBS Lett* 215: 327-330).

The following terms are used to describe the sequence relationships between two or more nucleic acids or polynucleotides: "reference sequence", "comparison window", "sequence identity", "percentage of sequence identity", and "substantial identity". A "reference sequence" is a defined sequence used as a basis for a sequence comparison; a reference sequence may be a subset of a larger sequence, for example, as a segment of a full-length cDNA or gene sequence given in a sequence listing, or may comprise a complete cDNA or gene sequence. Optimal alignment of sequences for aligning a comparison window may, for example, be conducted by the local homology algorithm of Smith and Waterman Adv. Appl. Math. 2482 (1981), by the homology alignment algorithm of Needleman and Wunsch J. Mol. Biol. 48:443 (1970), by the search for similarity method of Pearson and Lipman Proc. Natl. Acad. Sci. U.S.A. 852444 (1988), or by computerized implementations of these algorithms (for example, GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package Release 7.0, Genetics Computer Group, 575 Science Dr., Madison, WI).

Techniques for nucleic acid manipulation of the nucleic acid sequences harboring the cSNP's of the invention, such as subcloning nucleic acid sequences encoding polypeptides into expression vectors, labeling probes, DNA hybridization, and the like, are described generally in Sambrook et al., The phrase "nucleic acid sequence encoding" refers to a nucleic acid which directs the expression of a specific protein, peptide or amino acid sequence. The nucleic acid sequences include both the DNA strand sequence that is transcribed into RNA and the RNA sequence that is translated into protein, peptide or amino acid sequence. The nucleic acid sequences include both the full length nucleic acid sequences disclosed herein as well as non-full length sequences derived from the full length protein. It being further understood that the sequence includes the degenerate codons of the native sequence or sequences which may be introduced to provide codon preference in a specific host cell. Consequently, the principles of probe selection and array design can readily be extended to analyze more complex polymorphisms (see EP 730,663). For example, to characterize a triallelic SNP polymorphism, three groups of probes can be designed tiled on the three polymorphic forms as described above. As a further example, to analyze a diallelic polymorphism involving a deletion of a nucleotide, one can tile a first group of probes based

on the undeleted polymorphic form as the reference sequence and a second group of probes based on the deleted form as the reference sequence.

For assays of genomic DNA, virtually any biological convenient tissue sample can be used. Suitable samples include whole blood, semen, saliva, tears, urine, fecal material, sweat, buccal, skin and hair. Genomic DNA is typically amplified before analysis. Amplification is usually effected by PCR using primers flanking a suitable fragment e.g., of 50-500 nucleotides containing the locus of the polymorphism to be analyzed. Target is usually labeled in the course of amplification. The amplification product can be RNA or DNA, single stranded or double stranded. If double stranded, the amplification product is typically denatured before application to an array. If genomic DNA is analyzed without amplification, it may be desirable to remove RNA from the sample before applying it to the array. Such can be accomplished by digestion with DNase-free RNase.

DETECTION OF POLYMORPHISMS IN A NUCLEIC ACID SAMPLE

The SNPs disclosed herein can be used to determine which forms of a characterized polymorphism are present in individuals under analysis.

The design and use of allele-specific probes for analyzing polymorphisms is described by e.g., Saiki et al., Nature 324, 163-166 (1986); Dattagupta, EP 235,726, Saiki, WO 89/11548. Allele-specific probes can be designed that hybridize to a segment of target DNA from one individual but do not hybridize to the corresponding segment from another individual due to the presence of different polymorphic forms in the respective segments from the two individuals. Hybridization conditions should be sufficiently stringent that there is a significant difference in hybridization intensity between alleles, and preferably an essentially binary response, whereby a probe hybridizes to only one of the alleles. Some probes are designed to hybridize to a segment of target DNA such that the polymorphic site aligns with a central position (e.g., in a 15-mer at the 7 position; in a 16-mer, at either the 7, 8 or 9 position) of the probe. This design of probe achieves good discrimination in hybridization between different allelic forms.

Allele-specific probes are often used in pairs, one member of a pair showing a perfect match to a reference form of a target sequence and the other member showing a perfect match to a variant form. Several pairs of probes can then be immobilized on the same support for simultaneous analysis of multiple polymorphisms within the same target sequence.

The polymorphisms can also be identified by hybridization to nucleic acid arrays, some examples of which are described in published PCT application WO 95/11995. WO 95/11995 also describes subarrays that are optimized for detection of a variant form of a precharacterized polymorphism. Such a subarray contains probes designed to be complementary to a second reference sequence, which is an allelic variant of the first reference sequence. The second group of probes is designed by the same principles, except that the probes exhibit complementarity to the second reference sequence. The inclusion of a second group (or further groups) can be particularly useful for analyzing short subsequences of the primary reference sequence in which multiple mutations are expected to occur within a short distance commensurate with the length of the probes (e.g., two or more mutations within 9 to 21 bases).

An allele-specific primer hybridizes to a site on a target DNA overlapping a polymorphism and only primes amplification of an allelic form to which the primer exhibits perfect complementarity. See Gibbs, Nucleic Acid Res. 17 2427-2448 (1989). This primer is used in conjunction with a second primer which hybridizes at a distal site. Amplification proceeds from the two-primers, resulting in a detectable product which indicates the particular allelic form is present. A control is usually performed with a second pair of primers, one of which shows a single base mismatch at the polymorphic site and the other of which exhibits perfect complementarity to a distal site. The single-base mismatch prevents amplification and no detectable product is formed. The method works best when the mismatch is included in the 3'-most position of the oligonucleotide aligned with the polymorphism because this position is most destabilizing to elongation from the primer (see, e.g., WO 93/22456).

Amplification products generated using the polymerase chain reaction can be analyzed by the use of denaturing gradient gel electrophoresis. Different alleles can be identified based on the different sequence-dependent melting properties and electrophoretic migration of DNA in solution. Erlich, ed., PCR Technology, Principles and Applications for DNA Amplification, (W.H. Freeman and Co New York, 1992, Chapter 7).

Alleles of target sequences can be differentiated using single-strand conformation polymorphism analysis, which identifies base differences by alteration in electrophoretic migration of single stranded PCR products, as described in Orita et al., Proc. Nat. Acad. Sci. 86, 2766-2770 (1989). Amplified PCR products can be generated and heated or

otherwise denatured, to form single stranded amplification products. Single-stranded nucleic acids may refold or form secondary structures which are partially dependent on the base sequence. The different electrophoretic mobilities of single-stranded amplification products can be related to base-sequence differences between alleles of target sequences.

The genotype of an individual with respect to a pathology suspected of being caused by a genetic polymorphism may be assessed by association analysis. Phenotypic traits suitable for association analysis include diseases that have known but hitherto unmapped genetic components (e.g., agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial hypercholesterolemia, polycystic kidney disease, hereditary spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary hemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and acute intermittent porphyria).

Phenotypic traits also include symptoms of, or susceptibility to, multifactorial diseases of which a component is or may be genetic, such as autoimmune diseases, inflammation, cancer, diseases of the nervous system, and infection by pathogenic microorganisms. Some examples of autoimmune diseases include rheumatoid arthritis, multiple sclerosis, diabetes (insulin-dependent and non- independent), systemic lupus erythematosus and Graves disease. Some examples of cancers include cancers of the bladder, brain, breast, colon, esophagus, kidney, oral cavity, ovary, pancreas, prostate, skin, stomach, leukemia, liver, lung, and uterus. Phenotypic traits also include characteristics such as longevity, appearance (e.g., baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments.

Determination of which polymorphic forms occupy a set of polymorphic sites in an individual identifies a set of polymorphic forms that distinguishes the individual. See generally National Research Council, *The Evaluation of Forensic DNA Evidence* (Eds. Pollard et al., National Academy Press, DC, 1996). Since the polymorphic sites are within a 50,000 bp region in the human genome, the probability of recombination between these polymorphic sites is low. That low probability means the haplotype (the set of all 10 polymorphic sites) set forth in this application should be inherited without change for at least several generations. The more sites that are analyzed the lower the probability that the set of polymorphic forms in one individual is the same as that in an unrelated individual. Preferably, if multiple sites are analyzed, the sites are unlinked. Thus, polymorphisms of the

invention are often used in conjunction with polymorphisms in distal genes. Preferred polymorphisms for use in forensics are diallelic because the population frequencies of two polymorphic forms can usually be determined with greater accuracy than those of multiple polymorphic forms at multi-allelic loci.

The capacity to identify a distinguishing or unique set of forensic markers in an individual is useful for forensic analysis. For example, one can determine whether a blood sample from a suspect matches a blood or other tissue sample from a crime scene by determining whether the set of polymorphic forms occupying selected polymorphic sites is the same in the suspect and the sample. If the set of polymorphic markers does not match between a suspect and a sample, it can be concluded (barring experimental error) that the suspect was not the source of the sample. If the set of markers does match, one can conclude that the DNA from the suspect is consistent with that found at the crime scene. If frequencies of the polymorphic forms at the loci tested have been determined (e.g., by analysis of a suitable population of individuals), one can perform a statistical analysis to determine the probability that a match of suspect and crime scene sample would occur by chance.

p(ID) is the probability that two random individuals have the same polymorphic or allelic form at a given polymorphic site. In diallelic loci, four genotypes are possible: AA, AB, BA, and BB. If alleles A and B occur in a haploid genome of the organism with frequencies x and y, the probability of each genotype in a diploid organism are (see WO 95/12607):

Homozygote: $p(AA)=x^2$

Homozygote: $p(BB)=y^2=(1-x)^2$

Single Heterozygote: $p(AB)=p(BA)=xy=x(1-x)$

Both Heterozygotes: $p(AB+BA)=2xy=2x(1-x)$

The probability of identity at one locus (i.e, the probability that two individuals, picked at random from a population will have identical polymorphic forms at a given locus) is given by the equation:

$p(ID)=(x^2)^{2+}(2xy)^{2+}(y^2)^2$.

These calculations can be extended for any number of polymorphic forms at a given locus. For example, the probability of identity p(ID) for a 3-allele system where the alleles have the frequencies in the population of x, y and z, respectively, is equal to the sum of the squares of the genotype frequencies:

$$p(ID)=x^{4+}(2xy)^{2+}(2yz)^{2+}(2xz)^{2+}z^{4+}y^{4}$$

In a locus of n alleles, the appropriate binomial expansion is used to calculate p(ID) and p(exc).

The cumulative probability of identity (cum p(ID)) for each of multiple unlinked loci is determined by multiplying the probabilities provided by each locus:

$$cum\ p(ID)=p(ID1)p(ID2)p(ID3)\ldots p(IDn)$$

The cumulative probability of non-identity for n loci (i.e. the probability that two random individuals will be different at 1 or more loci) is given by the equation:

$$cum\ p(nonID)=1-cum\ p(ID).$$

If several polymorphic loci are tested, the cumulative probability of non-identity for random individuals becomes very high (e.g., one billion to one). Such probabilities can be taken into account together with other evidence in determining the guilt or innocence of the suspect.

The object of paternity testing is usually to determine whether a male is the father of a child. In most cases, the mother of the child is known and thus, the mother's contribution to the child's genotype can be traced. Paternity testing investigates whether the part of the child's genotype not attributable to the mother is consistent with that of the putative father. Paternity testing can be performed by analyzing sets of polymorphisms in the putative father and the child.

If the set of polymorphisms in the child attributable to the father does not match the putative father, it can be concluded, barring experimental error, that the putative father is not the real father. If the set of polymorphisms in the child attributable to the father does match the set of polymorphisms of the putative father, a statistical calculation can be performed to determine the probability of coincidental match.

The probability of parentage exclusion (representing the probability that a random male will have a polymorphic form at a given polymorphic site that makes him incompatible as the father) is given by the equation (see WO 95/12607):

$p(exc)=xy(1-xy)$

where x and y are the population frequencies of alleles A and B of a diallelic polymorphic site. (At a triallelic site p(exc)=xy(1-xy)+ yz(1-yz)+ xz(1-xz)+ 3xyz(1-xyz))), where x, y and z and the respective population frequencies of alleles A, B and C). The probability of non-exclusion is:

$p(non\text{-}exc)=1-p(exc)$

The cumulative probability of non-exclusion (representing the value obtained when n loci are used) is thus:

$cum\ p(non\text{-}exc)=p(non\text{-}exc1)p(non\text{-}exc2)p(non\text{-}exc3)\ldots p(non\text{-}excn)$

The cumulative probability of exclusion for n loci (representing the probability that a random male will be excluded) is:

$cum\ p(exc)=1-cum\ p(non\text{-}exc).$

If several polymorphic loci are included in the analysis, the cumulative probability of exclusion of a random male is very high. This probability can be taken into account in assessing the liability of a putative father whose polymorphic marker set matches the child's polymorphic marker set attributable to his/her father.

The polymorphisms of the invention may contribute to the phenotype of an organism in different ways. Some polymorphisms occur within a protein coding sequence and contribute to phenotype by affecting protein structure. The effect may be neutral, beneficial or detrimental, or both beneficial and detrimental, depending on the circumstances. For example, a heterozygous sickle cell mutation confers resistance to malaria, but a homozygous sickle cell mutation is usually lethal. Other polymorphisms occur in noncoding regions but may exert phenotypic effects indirectly via influence on replication, transcription, and translation. A single polymorphism may affect more than one phenotypic trait. Likewise, a single phenotypic trait may be affected by polymorphisms in different genes. Further, some

polymorphisms predispose an individual to a distinct mutation that is causally related to a certain phenotype.

Phenotypic traits include diseases that have known but hitherto unmapped genetic components. Phenotypic traits also include symptoms of, or susceptibility to, multifactorial diseases of which a component is or may be genetic, such as autoimmune diseases, inflammation, cancer, diseases of the nervous system, and infection by pathogenic microorganisms. Some examples of autoimmune diseases include rheumatoid arthritis, multiple sclerosis, diabetes (insulin-dependent and non-independent), systemic lupus erythematosus and Graves disease. Some examples of cancers include cancers of the bladder, brain, breast, colon, esophagus, kidney, leukemia, liver, lung, oral cavity, ovary, pancreas, prostate, skin, stomach and uterus. Phenotypic traits also include characteristics such as longevity, appearance (e.g., baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments.

Correlation is performed for a population of individuals who have been tested for the presence or absence of a phenotypic trait of interest and for polymorphic marker sets. To perform such analysis, the presence or absence of a set of polymorphisms (i.e. a polymorphic set) is determined for a set of the individuals, some of whom exhibit a particular trait, and some of whom exhibit lack of the trait. The alleles of each polymorphism of the set are then reviewed to determine whether the presence or absence of a particular allele is associated with the trait of interest. Correlation can be performed by standard statistical methods and statistically significant correlations between polymorphic form(s) and phenotypic characteristics are noted. For example, it might be found that the presence of allele A1 at polymorphism A correlates with heart disease. As a further example, it might be found that the combined presence of allele A1 at polymorphism A and allele B1 at polymorphism B correlates with increased milk production of a farm animal.

Such correlations can be exploited in several ways. In the case of a strong correlation between a set of one or more polymorphic forms and a disease for which treatment is available, detection of the polymorphic form set in a human or animal patient may justify immediate administration of treatment, or at least the institution of regular monitoring of the patient. Detection of a polymorphic form correlated with serious disease in a couple contemplating a family may also be valuable to the couple in their reproductive decisions. For example, the female partner might elect to undergo in vitro fertilization to avoid the

possibility of transmitting such a polymorphism from her husband to her offspring. In the case of a weaker, but still statistically significant correlation between a polymorphic set and human disease, immediate therapeutic intervention or monitoring may not be justified. Nevertheless, the patient can be motivated to begin simple life-style changes (e.g., diet, exercise) that can be accomplished at little cost to the patient but confer potential benefits in reducing the risk of conditions to which the patient may have increased susceptibility by virtue of variant alleles. Identification of a polymorphic set in a patient correlated with enhanced receptiveness to one of several treatment regimes for a disease indicates that this treatment regime should be followed.

For animals and plants, correlations between characteristics and phenotype are useful for breeding for desired characteristics. For example, Beitz et al., U.S. Pat. No. 5,292,639 discuss use of bovine mitochondrial polymorphisms in a breeding program to improve milk production in cows. To evaluate the effect of mtDNA D-loop sequence polymorphism on milk production, each cow was assigned a value of 1 if variant or 0 if wild type with respect to a prototypical mitochondrial DNA sequence at each of 17 locations considered.

The previous section concerns identifying correlations between phenotypic traits and polymorphisms that directly or indirectly contribute to those traits. The present section describes identification of a physical linkage between a genetic locus associated with a trait of interest and polymorphic markers that are not associated with the trait, but are in physical proximity with the genetic locus responsible for the trait and co-segregate with it. Such analysis is useful for mapping a genetic locus associated with a phenotypic trait to a chromosomal position, and thereby cloning gene(s) responsible for the trait. See Lander et al., *Proc. Natl. Acad. Sci.* (USA) 83, 7353-7357 (1986); Lander et al., *Proc. Natl. Acad. Sci.* (USA) 84, 2363-2367 (1987); Donis-Keller et al., *Cell* 51, 319-337 (1987); Lander et al., *Genetics* 121, 185-199 (1989)). Genes localized by linkage can be cloned by a process known as directional cloning. See Wainwright, *Med. J. Australia* 159, 170-174 (1993); Collins, *Nature Genetics* 1, 3-6 (1992) (each of which is incorporated by reference in its entirety for all purposes).

Linkage studies are typically performed on members of a family. Available members of the family are characterized for the presence or absence of a phenotypic trait and for a set of polymorphic markers. The distribution of polymorphic markers in an informative meiosis is then analyzed to determine which polymorphic markers co-segregate with a phenotypic

trait. See, e.g., Kerem et al., *Science* 245, 1073-1080 (1989); Monaco et al., *Nature* 316, 842 (1985); Yamoka et al., *Neurology* 40, 222-226 (1990); Rossiter et al., *FASEB Journal* 5, 21-27 (1991).

Linkage is analyzed by calculation of LOD (log of the odds) values. A lod value is the relative likelihood of obtaining observed segregation data for a marker and a genetic locus when the two are located at a recombination fraction *RF*, versus the situation in which the two are not linked, and thus segregating independently (Thompson & Thompson, *Genetics in Medicine* (5th ed, W.B. Saunders Company, Philadelphia, 1991); Strachan, "Mapping the human genome" in *The Human Genome* (BIOS Scientific Publishers Ltd, Oxford), Chapter 4). A series of likelihood ratios are calculated at various recombination fractions (*RF*), ranging from *RF*=0.0 (coincident loci) to *RF*=0.50 (unlinked). Thus, the likelihood at a given value of *RF* is: probability of data if loci linked at *RF* to probability of data if loci unlinked. The computed likelihood is usually expressed as the $\log_{10}$ of this ratio (i.e., a lod score). For example, a lod score of 3 indicates 1000:1 odds against an apparent observed linkage being a coincidence. The use of logarithms allows data collected from different families to be combined by simple addition. Computer programs are available for the calculation of lod scores for differing values of *RF* (e.g., LIPED, MLINK (Lathrop, *Proc. Nat. Acad. Sci.* (USA) 81, 3443-3446 (1984)). For any particular lod score, a recombination fraction may be determined from mathematical tables. See Smith et al., *Mathematical tables for research workers in human genetics* (Churchill, London, 1961); Smith, *Ann. Hum. Genet.* 32, 127-150 (1968). The value of *RF* at which the lod score is the highest is considered to be the best estimate of the recombination fraction.

Positive lod score values suggest that the two loci are linked, whereas negative values suggest that linkage is less likely (at that value of *RF*) than the possibility that the two loci are unlinked. By convention, a combined lod score of + 3 or greater (equivalent to greater than 1000:1 odds in favor of linkage) is considered definitive evidence that two loci are linked. Similarly, by convention, a negative lod score of -2 or less is taken as definitive evidence against linkage of the two loci being compared. Negative linkage data are useful in excluding a chromosome or a segment thereof from consideration. The search focuses on the remaining non-excluded chromosomal locations.

The invention further provides transgenic nonhuman animals capable of expressing an exogenous variant gene and/or having one or both alleles of an endogenous variant gene

inactivated. Expression of an exogenous variant gene is usually achieved by operably linking the gene to a promoter and optionally an enhancer, and microinjecting the construct into a zygote. See Hogan et al., "Manipulating the Mouse Embryo, A Laboratory Manual," Cold Spring Harbor Laboratory. (1989). Inactivation of endogenous variant genes can be achieved by forming a transgene in which a cloned variant gene is inactivated by insertion of a positive selection marker. See Capecchi, Science 244, 1288-1292 The transgene is then introduced into an embryonic stem cell, where it undergoes homologous recombination with an endogenous variant gene. Mice and other rodents are preferred animals. Such animals provide useful drug screening systems.

The invention further provides methods for assessing the pharmacogenomic susceptibility of a subject harboring a single nucleotide polymorphism to a particular pharmaceutical compound, or to a class of such compounds. Genetic polymorphism in drug-metabolizing enzymes, drug transporters, receptors for pharmaceutical agents, and other drug targets have been correlated with individual differences based on distinction in the efficacy and toxicity of the pharmaceutical agent administered to a subject. Pharmocogenomic characterization of a subjects susceptibility to a drug enhances the ability to tailor a dosing regimen to the particular genetic constitution of the subject, thereby enhancing and optimizing the therapeutic effectiveness of the therapy.

In cases in which a cSNP leads to a polymorphic protein that is ascribed to be the cause of a pathological condition, method of treating such a condition includes administering to a subject experiencing the pathology the wild type cognate of the polymorphic protein. Once administered in an effective dosing regimen, the wild type cognate provides complementation or remediation of the defect due to the polymorphic protein. The subject's condition is ameliorated by this protein therapy.

A subject suspected of suffering from a pathology ascribable to a polymorphic protein that arises from a cSNP is to be diagnosed using any of a variety of diagnostic methods capable of identifying the presence of the cSNP in the nucleic acid, or of the cognate polymorphic protein, in a suitable clinical sample taken from the subject. Once the presence of the cSNP has been ascertained, and the pathology is correctable by administering a normal or wild-type gene, the subject is treated with a pharmaceutical composition that includes a nucleic acid that harbors the correcting wild-type gene, or a fragment containing a correcting sequence of the wild-type gene. Non-limiting examples of ways in which such a nucleic acid

may be administered include incorporating the wild-type gene in a viral vector, such as an adenovirus or adeno associated virus, and administration of a naked DNA in a pharmaceutical composition that promotes intracellular uptake of the administered nucleic acid. Once the nucleic acid that includes the gene coding for the wild-type allele of the polymorphism is incorporated within a cell of the subject, it will initiate *de novo* biosynthesis of the wild-type gene product. If the nucleic acid is further incorporated into the genome of the subject, the treatment will have long-term effects, providing *de novo* synthesis of the wild-type protein for a prolonged duration. The synthesis of the wild-type protein in the cells of the subject will contribute to a therapeutic enhancement of the clinical condition of the subject.

A subject suffering from a pathology ascribed to a SNP may be treated so as to correct the genetic defect. (See Kren et al., Proc. Natl. Acad. Sci. USA 96:10349-10354 (1999)). Such a subject is identified by any method that can detect the polymorphism in a sample drawn from the subject. Such a genetic defect may be permanently corrected by administering to such a subject a nucleic acid fragment incorporating a repair sequence that supplies the wild-type nucleotide at the position of the SNP. This site-specific repair sequence encompasses an RNA/DNA oligonucleotide which operates to promote endogenous repair of a subject's genomic DNA. Upon administration in an appropriate vehicle, such as a complex with polyethylenimine or encapsulated in anionic liposomes, a genetic defect leading to an inborn pathology may be overcome, as the chimeric oligonucleotides induces incorporation of the wild-type sequence into the subject's genome. Upon incorporation, the wild-type gene product is expressed, and the replacement is propagated, thereby engendering a permanent repair.

The invention further provides kits comprising at least one allele-specific oligonucleotide as described above. Often, the kits contain one or more pairs of allele-specific oligonucleotides hybridizing to different forms of a polymorphism. In some kits, the allele-specific oligonucleotides are provided immobilized to a substrate. For example, the same substrate can comprise allele-specific oligonucleotide probes for detecting at least 10, 100, 1000 or all of the polymorphisms shown in the Table. Optional additional components of the kit include, for example, restriction enzymes, reverse-transcriptase or polymerase, the substrate nucleoside triphosphates, means used to label (for example, an avidin-enzyme conjugate and enzyme substrate and chromogen if the label is biotin), and the appropriate buffers for reverse transcription, PCR, or hybridization reactions. Usually, the kit also contains instructions for carrying out the hybridizing methods.

Several aspects of the present invention rely on having available the polymorphic proteins encoded by the nucleic acids comprising a SNP of the inventions. There are various methods of isolating these nucleic acid sequences. For example, DNA is isolated from a genomic or cDNA library using labeled oligonucleotide probes having sequences complementary to the sequences disclosed herein.

Such probes can be used directly in hybridization assays. Alternatively probes can be designed for use in amplification techniques such as PCR.

To prepare a cDNA library, mRNA is isolated from tissue such as heart or pancreas, preferably a tissue wherein expression of the gene or gene family is likely to occur. cDNA is prepared from the mRNA and ligated into a recombinant vector. The vector is transfected into a recombinant host for propagation, screening and cloning. Methods for making and screening cDNA libraries are well known, See Gubler, U. and Hoffman, B.J. Gene 25:263-269 (1983) and Sambrook et al.

For a genomic library, for example, the DNA is extracted from tissue and either mechanically sheared or enzymatically digested to yield fragments of about 12-20 kb. The fragments are then separated by gradient centrifugation from undesired sizes and are constructed in bacteriophage lambda vectors. These vectors and phage are packaged *in vitro,* as described in Sambrook, et al. Recombinant phage are analyzed by plaque hybridization as described in Benton and Davis, Science 196:180-l 82 (1977). Colony hybridization is carried out as generally described in M. Grunstein et al. Proc. Natl. Acad. Sci. USA. 72:3961-3965 (1975). DNA of interest is identified in either cDNA or genomic libraries by its ability to hybridize with nucleic acid probes, for example on Southern blots, and these DNA regions are isolated by standard methods familiar to those of skill in the art. See Sambrook, et al.

In PCR techniques, oligonucleotide primers complementary to the two 3' borders of the DNA region to be amplified are synthesized. The polymerase chain reaction is then carried out using the two primers. See PCR Protocols: a Guide to Methods and Applications (Innis, M, Gelfand, D., Sninsky, J. and White, T., eds.), Academic Press, San Diego (1990). Primers can be selected to amplify the entire regions encoding a full-length sequence of interest or to amplify smaller DNA segments as desired. PCR can be used in a variety of protocols to isolate cDNAs encoding a sequence of interest. In these protocols, appropriate primers and probes for amplifying DNA encoding a sequence of interest are generated from

analysis of the DNA sequences listed herein. Once such regions are PCR-amplified, they can be sequenced and oligonucleotide probes can be prepared from the sequence.

Once DNA encoding a sequence comprising a cSNP is isolated and cloned, one can express the encoded polymorphic proteins in a variety of recombinantly engineered cells. It is expected that those of skill in the art are knowledgeable in the numerous expression systems available for expression of DNA encoding a sequence of interest. No attempt to describe in detail the various methods known for the expression of proteins in prokaryotes or eukaryotes is made here.

In brief summary, the expression of natural or synthetic nucleic acids encoding a sequence of interest will typically be achieved by operably linking the DNA or cDNA to a promoter (which is either constitutive or inducible), followed by incorporation into an expression vector. The vectors can be suitable for replication and integration in either prokaryotes or eukaryotes. Typical expression vectors contain initiation sequences, transcription and translation terminators, and promoters useful for regulation of the expression of a polynucleotide sequence of interest. To obtain high level expression of a cloned gene, it is desirable to construct expression plasmids which contain, at the minimum, a strong promoter to direct transcription, a ribosome binding site for translational initiation, and a transcription/translation terminator. The expression vectors may also comprise generic expression cassettes containing at least one independent terminator sequence, sequences permitting replication of the plasmid in both eukaryotes and prokaryotes, i.e., shuttle vectors, and selection markers for both prokaryotic and eukaryotic systems. See Sambrook et al.

A variety of prokaryotic expression systems may be used to express the polymorphic proteins of the invention. Examples include *E. coli*, Bacillus, Streptomyces, and the like.

It is preferred to construct expression plasmids which contain, at the minimum, a strong promoter to direct transcription, a ribosome binding site for translational initiation, and a transcription/translation terminator. Examples of regulatory regions suitable for this purpose in *E. coli* are the promoter and operator region of the *E. coli* tryptophan biosynthetic pathway as described by Yanofsky, C., J. Bacterial. 158:1018-1024 (1984) and the leftward promoter of phage lambda as described by Λ, I. and Hagen, D., Ann. Rev. Genet. 14:399-445 (1980). The inclusion of selection markers in DNA vectors transformed in *E. coli* is also useful. Examples of such markers include genes specifying resistance to ampicillin,

tetracycline, or chloramphenicol. See Sambrook et al. for details concerning selection markers for use in *E. coli.*

To enhance proper folding of the expressed recombinant protein, during purification from *E. coli*, the expressed protein may first be denatured and then renatured. This can be accomplished by solubilizing the bacterially produced proteins in a chaotropic agent such as guanidine HCI and reducing all the cysteine residues with a reducing agent such as beta-mercaptoethanol. The protein is then renatured, either by slow dialysis or by gel filtration. See U.S. Patent No. 4,511,503. Detection of the expressed antigen is achieved by methods known in the art as radioimmunoassay, or Western blotting techniques or immunoprecipitation. Purification from *E. coli* can be achieved following procedures such as those described in U.S. Patent No. 4,511,503.

Any of a variety of eukaryotic expression systems such as yeast, insect cell lines, bird, fish, and mammalian cells, may also be used to express a polymorphic protein of the invention. As explained briefly below, a nucleotide sequence harboring a cSNP may be expressed in these eukaryotic systems. Synthesis of heterologous proteins in yeast is well known. Methods in Yeast Genetics, Sherman, F., et al., Cold Spring Harbor Laboratory, (1982) is a well recognized work describing the various methods available to produce the protein in yeast. Suitable vectors usually have expression control sequences, such as promoters, including 3-phosphogtycerate kinase or other glycolytic enzymes, and an origin of replication, termination sequences and the like as desired. For instance, suitable vectors are described in the literature (Botstein, et al., Gene 8:17-24 (1979); Broach, et al., Gene 8:121-133 (1979)).

Two procedures are used in transforming yeast cells. In one case, yeast cells are first converted into protoplasts using zymolyase, lyticase or glusulase, followed by addition of DNA and polyethylene glycol (PEG). The PEG-treated protoplasts are then regenerated in a 3% agar medium under selective conditions. Details of this procedure are given in the papers by J.D. Beggs, Nature (London) 275:104-109 (1978); and Hinnen, A., et al., Proc. Natl. Acad. Sci. USA, 75:1929-1933 (1978). The second procedure does not involve removal of the cell wall. Instead the cells are treated with lithium chloride or acetate and PEG and put on selective plates (Ito, H., et al., J. Bact, 153163-168 (1983)) cells and applying standard protein isolation techniques to the lysates:.

The purification process can be monitored by using Western blot techniques or radioimmunoassay or other standard techniques. The sequences encoding the proteins of the invention can also be ligated to various immunoassay expression vectors for use in transforming cell cultures of, for instance, mammalian, insect, bird or fish origin. Illustrative of cell cultures useful for the production of the polypeptides are mammalian cells. Mammalian cell systems often will be in the form of monolayers of cells although mammalian cell suspensions may also be used. A number of suitable host cell lines capable of expressing intact proteins have been developed in the art, and include the HEK293, BHK21, and CHO cell lines, and various human cells such as COS cell lines, HeLa cells, myeloma cell lines, Jurkat cells, etc. Expression vectors for these cells can include expression control sequences, such as an origin of replication, a promoter (e.g., the CMV promoter, a HSV *tk* promoter or *pgk* (phosphoglycerate kinase) promoter), an enhancer (Queen et al. Immunol. Rev. 89:49 (1986)) and necessary processing information sites, such as ribosome binding sites, RNA splice sites, polyadenylation sites (e.g., an SV40 large T Ag poly A addition site), and transcriptional terminator sequences.

Other animal cells are available, for instance, from the American Type Culture Collection Catalogue of Cell Lines and Hybridomas (7th edition, (1992)). Appropriate vectors for expressing the proteins of the invention in insect cells are usually derived from baculovirus. Insect cell lines include mosquito larvae, silkworm, armyworm, moth and Drosophila cell lines such as a Schneider cell line (See Schneider J. Embryol. Exp. Morphol., 27:353-365 (1987). As indicated above, the vector, e.g., a plasmid, which is used to transform the host cell, preferably contains DNA sequences to initiate transcription and sequences to control the translation of the protein. These sequences are referred to as expression control sequences. As with yeast, when higher animal host cells are employed, polyadenylation or transcription terminator sequences from known mammalian genes need to be incorporated into the vector. An example of a terminator sequence is the polyadenylation sequence from the bovine growth hormone gene. Sequences for accurate splicing of the transcript may also be included. An example of a splicing sequence is the VP1 intron from SV4O (Sprague, J. et a/., J. Virol. 45: 773-781 (1983)). Additionally, gene sequences to control replication in the host cell may be Saveria-Campo, M., 1985, "Bovine Papilloma virus DNA a Eukaryotic Cloning Vector" in DNA Cloning Vol. II a Practical Approach Ed. D.M. Glover, IRL Press, Arlington, Virginia pp. 213-238. The host cells are competent or rendered competent for transformation by various means. There are several well-known

methods of introducing DNA into animal cells. These include: calcium phosphate precipitation, fusion of the recipient cells with bacterial protoplasts containing the DNA, treatment of the recipient cells with liposomes containing the DNA, DEAE dextran, electroporation and micro-injection of the DNA directly into the cells.

The transformed cells are cultured by means well known in the art (Biochemical Methods in Cell Culture and Virology, Kuchler, R.J., Dowden, Hutchinson and Ross, Inc., (1977)). The expressed polypeptides are isolated from cells grown as suspensions or as monolayers. The latter are recovered by well known mechanical, chemical or enzymatic means.

General methods of expressing recombinant proteins are also known and are exemplified in R. Kaufman, Methods in Enzymology 185, 537-566 (1990). As defined herein "operably linked" refers to linkage of a promoter upstream from a DNA sequence such that the promoter mediates transcription of the DNA sequence. Specifically, "operably linked" means that the isolated polynucleotide of the invention and an expression control sequence are situated within a vector or cell in such a way that the gene encoding the protein is expressed by a host cell which has been transformed (transfected) with the ligated polynucleotide/expression sequence. The term "vector", refers to viral expression systems, autonomous self-replicating circular DNA (plasmids), and includes both expression and nonexpression plasmids.

The term "gene" as used herein is intended to refer to a nucleic acid sequence which encodes a polypeptide. This definition includes various sequence polymorphisms, mutations, and/or sequence variants wherein such alterations do not affect the function of the gene product. The term "gene" is intended to include not only coding sequences but also regulatory regions such as promoters, enhancers, termination regions and similar untranslated nucleotide sequences. The term further includes all introns and other DNA sequences spliced from the mRNA transcript, along with variants resulting from alternative splice sites.

A number of types of cells may act as suitable host cells for expression of the protein. Mammalian host cells include, for example, monkey COS cells, Chinese Hamster Ovary (CHO) cells, human kidney 293 cells, human epidermal A43 1 cells, human Co10205 cells, 3T3 cells, CV-1 cells, other transformed primate cell lines, normal diploid cells, cell strains derived from in vitro culture of primary tissue, primary explants, HeLa cells, mouse L cells,

BHK, HL- 60, U937, HaK or Jurkat cells. Alternatively, it may be possible to produce the protein in lower eukaryotes such as yeast or in prokaryotes such as bacteria. Potentially suitable yeast strains include *Saccharomyces cerevisiae, Schizosaccharomyces pombe, Kluyveromyces* strains, Candida or any yeast strain capable of expressing heterologous proteins. Potentially suitable bacterial strains include *Escherichia coli, Bacillus subtilis, Salmonella typhimurium,* or any bacterial strain capable of expressing heterologous proteins. If the protein is made in yeast or bacteria, it may be necessary to modify the protein produced therein, for example by phosphorylation or glycosylation of the appropriate sites, in order to obtain the functional protein.

The protein may also be produced by operably linking the isolated polynucleotide of the invention to suitable control sequences in one or more insect expression vectors, and employing an insect expression system. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, e.g., Invitrogen, San Diego, California, U.S.A. (the MaxBac© kit), and such methods are well known in the art, as described in Summers and Smith, Texas Agricultural Experiment Station Bulletin No. 1555 (1987), incorporated herein by reference. As used herein, an insect cell capable of expressing a polynucleotide of the present invention is "transformed." The protein of the invention may be prepared by culturing transformed host cells under culture conditions suitable to express the recombinant protein.

The polymorphic protein of the invention may also be expressed as a product of transgenic animals, e.g., as a component of the milk of transgenic cows, goats, pigs, or sheep which are characterized by somatic or germ cells containing a nucleotide sequence encoding the protein. The protein may also be produced by known conventional chemical synthesis. Methods for constructing the proteins of the present invention by synthetic means are known to those skilled in the art.

The polymorphic proteins produced by recombinant DNA technology may be purified by techniques commonly employed to isolate or purify recombinant proteins. Recombinantly produced proteins can be directly expressed or expressed as a fusion protein. The protein is then purified by a combination of cell lysis (e.g., sonication) and affinity chromatography. For fusion products, subsequent digestion of the fusion protein with an appropriate proteolytic enzyme releases the desired polypeptide. The polypeptides of this invention may be purified to substantial purity by standard techniques well known in the art, including

selective precipitation with such substances as ammonium sulfate, column chromatography, immunopurification methods, and others. See, for instance, R. Scopes, Protein Purification: Principles and Practice, Springer-Verlag: New York (1982), incorporated herein by reference. For example, in an embodiment, antibodies may be raised to the proteins of the invention as described herein. Cell membranes are isolated from a cell line expressing the recombinant protein, the protein is extracted from the membranes and immunoprecipitated. The proteins may then be further purified by standard protein chemistry techniques as described above.

The resulting expressed protein may then be purified from such culture (i.e., from culture medium or cell extracts) using known purification processes, such as gel filtration and ion exchange chromatography. The purification of the protein may also include an affinity column containing agents which will bind to the protein; one or more column steps over such affinity resins as concanavalin A-agarose, heparin-Toyopearl@ or Cibacrom blue 3GA Sepharose B; one or more steps involving hydrophobic interaction chromatography using such resins as phenyl ether, butyl ether, or propyl ether; or immunoaffinity chromatography. Alternatively, the protein of the invention may also be expressed in a form which will facilitate purification. For example, it may be expressed as a fusion protein, such as those of maltose binding protein (MBP), glutathione-S-transferase (GST) or thioredoxin (TRX). Kits for expression and purification of such fusion proteins are commercially available from New England BioLab (Beverly, MA), Pharmacia (Piscataway, NJ) and InVitrogen, respectively. The protein can also be tagged with an epitope and subsequently purified by using a specific antibody directed to such epitope. One such epitope ("Flag") is commercially available from Kodak (New Haven, CT). Finally, one or more reverse-phase high performance liquid chromatography (RP- HPLC) steps employing hydrophobic RP-HPLC media, e.g., silica gel having pendant methyl or other aliphatic groups, can be employed to further purify the protein. Some or all of the foregoing purification steps, in various combinations, can also be employed to provide a substantially homogeneous isolated recombinant protein. The protein thus purified is substantially free of other mammalian proteins and is defined in accordance with the present invention as an "isolated protein."

The term "antibody" as used herein refers to immunoglobulin molecules and immunologically active portions of immunoglobulin molecules, *i.e.*, molecules that contain an antigen binding site that specifically binds (immunoreacts with) an antigen, such as polymorphic. Such antibodies include, but are not limited to, polyclonal, monoclonal,

chimeric, single chain, F_{ab} and $F_{(ab')2}$ fragments, and an F_{ab} expression library. In a specific embodiment, antibodies to human polymorphic proteins are disclosed.

The phrase "specifically binds to", "immunospecifically binds to" or is "specifically immunoreactive with", an antibody when referring to a protein or peptide, refers to a binding reaction which is determinative of the presence of the protein in the presence of a heterogeneous population of proteins and other biological materials. Thus, for example, under designated immunoassay conditions, the specified antibodies bind to a particular protein and do not bind in a significant amount to other proteins present in the sample. Specific binding to an antibody under such conditions may require an antibody that is selected for its specificity for a particular protein. Of particular interest in the present invention is an antibody that binds immunospecifically to a polymorphic protein but not to its cognate wild type allelic protein, or vice versa. A variety of immunoassay formats may be used to select antibodies specifically immunoreactive with a particular protein. For example, solid-phase ELISA immunoassays are routinely used to select monoclonal antibodies specifically immunoreactive with a protein. See Harlow and Lane (1988) Antibodies, a Laboratory Manual, Cold Spring Harbor Publications, New York, for a description of immunoassay formats and conditions that can be used to determine specific immunoreactivity.

Polyclonal and/or monoclonal antibodies that immunospecifically bind to polymorphic gene products but not to the corresponding prototypical or "wild-type" gene products are also provided. Antibodies can be made by injecting mice or other animals with the variant gene product or synthetic peptide. Monoclonal antibodies are screened as are described, for example, in Harlow & Lane, Antibodies, A Laboratory Manual, Cold Spring Harbor Press, New York (1988); Goding, Monoclonal antibodies, Principles and Practice (2d ed.) Academic Press, New York (1986). Monoclonal antibodies are tested for specific immunoreactivity with a variant gene product and lack of immunoreactivity to the corresponding prototypical gene product.

An isolated polymorphic protein, or a portion or fragment thereof, can be used as an immunogen to generate the antibody that binds the polymorphic protein using standard techniques for polyclonal and monoclonal antibody preparation. The full-length polymorphic protein can be used or, alternatively, the invention provides antigenic peptide fragments of polymorphic for use as immunogens. The antigenic peptide of a polymorphic protein of the

invention comprises at least 8 amino acid residues of the amino acid sequence encompassing the polymorphic amino acid and encompasses an epitope of the polymorphic protein such that an antibody raised against the peptide forms a specific immune complex with the polymorphic protein. Preferably, the antigenic peptide comprises at least 10 amino acid residues, more preferably at least 15 amino acid residues, even more preferably at least 20 amino acid residues, and most preferably at least 30 amino acid residues. Preferred epitopes encompassed by the antigenic peptide are regions of polymorphic that are located on the surface of the protein, *e.g.*, hydrophilic regions.

For the production of polyclonal antibodies, various suitable host animals (*e.g.*, rabbit, goat, mouse or other mammal) may be immunized by injection with the polymorphic protein. An appropriate immunogenic preparation can contain, for example, recombinantly expressed polymorphic protein or a chemically synthesized polymorphic polypeptide. The preparation can further include an adjuvant. Various adjuvants used to increase the immunological response include, but are not limited to, Freund's (complete and incomplete), mineral gels (*e.g.*, aluminum hydroxide), surface active substances (*e.g.*, lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, dinitrophenol, etc.), human adjuvants such as *Bacille Calmette-Guerin* and *Corynebacterium parvum*, or similar immunostimulatory agents. If desired, the antibody molecules directed against polymorphic proteins can be isolated from the mammal (*e.g.*, from the blood) and further purified by well known techniques, such as protein A chromatography, to obtain the IgG fraction.

The term "monoclonal antibody" or "monoclonal antibody composition", as used herein, refers to a population of antibody molecules that originates from the clone of a singly hybridoma cell, and that contains only one type of antigen binding site capable of immunoreacting with a particular epitope of a polymorphic protein. A monoclonal antibody composition thus typically displays a single binding affinity for a particular polymorphic protein with which it immunoreacts. For preparation of monoclonal antibodies directed towards a particular polymorphic protein, or derivatives, fragments, analogs or homologs thereof, any technique that provides for the production of antibody molecules by continuous cell line culture may be utilized. Such techniques include, but are not limited to, the hybridoma technique (see Kohler & Milstein, 1975 *Nature* 256: 495-497); the trioma technique; the human B-cell hybridoma technique (see Kozbor, *et al.*, 1983 *Immunol Today* 4: 72) and the EBV hybridoma technique to produce human monoclonal antibodies (see Cole, *et al.*, 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp.

77-96). Human monoclonal antibodies may be utilized in the practice of the present invention and may be produced by using human hybridomas (see Cote, *et al.*, 1983. *Proc Natl Acad Sci USA* 80: 2026-2030) or by transforming human B-cells with Epstein Barr Virus *in vitro* (see Cole, *et al.*, 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96).

According to the invention, techniques can be adapted for the production of single-chain antibodies specific to a polymorphic protein (see *e.g.*, U.S. Patent No. 4,946,778). In addition, methodologies can be adapted for the construction of F_{ab} expression libraries (see *e.g.*, Huse, *et al.*, 1989 *Science* 246: 1275-1281) to allow rapid and effective identification of monoclonal F_{ab} fragments with the desired specificity for a polymorphic protein or derivatives, fragments, analogs or homologs thereof. Non-human antibodies can be "humanized" by techniques well known in the art. See *e.g.*, U.S. Patent No. 5,225,539. Antibody fragments that contain the idiotypes to a polymorphic protein may be produced by techniques known in the art including, but not limited to: (*i*) an $F_{(ab')2}$ fragment produced by pepsin digestion of an antibody molecule; (*ii*) an F_{ab} fragment generated by reducing the disulfide bridges of an $F_{(ab')2}$ fragment; (*iii*) an F_{ab} fragment generated by the treatment of the antibody molecule with papain and a reducing agent and (*iv*) F_v fragments.

Additionally, recombinant anti-polymorphic protein antibodies, such as chimeric and humanized monoclonal antibodies, comprising both human and non-human portions, which can be made using standard recombinant DNA techniques, are within the scope of the invention. Such chimeric and humanized monoclonal antibodies can be produced by recombinant DNA techniques known in the art, for example using methods described in PCT International Application No. PCT/US86/02269; European Patent Application No. 184,187; European Patent Application No. 171,496; European Patent Application No. 173,494; PCT

In one embodiment, methodologies for the screening of antibodies that possess the desired specificity include, but are not limited to, enzyme-linked immunosorbent assay (ELISA) and other immunologically-mediated techniques known within the art.

Anti-polymorphic protein antibodies may be used in methods known within the art relating to the detection, quantitation and/or cellular or tissue localization of a polymorphic protein (*e.g.*, for use in measuring levels of the polymorphic protein within appropriate physiological samples, for use in diagnostic methods, for use in imaging the protein, and the like). In a given embodiment, antibodies for polymorphic proteins, or derivatives, fragments, analogs or homologs thereof, that contain the antibody-derived CDR, are utilized as pharmacologically-active compounds in therapeutic applications intended to treat a pathology in a subject that arises from the presence of the cSNP allele in the subject.

An anti-polymorphic protein antibody (*e.g.*, monoclonal antibody) can be used to isolate polymorphic proteins by a variety of immunochemical techniques, such as immunoaffinity chromatography or immunoprecipitation. An anti-polymorphic protein antibody can facilitate the purification of natural polymorphic protein from cells and of recombinantly produced polymorphic proteins expressed in host cells. Moreover, an anti-polymorphic protein antibody can be used to detect polymorphic protein (*e.g.*, in a cellular lysate or cell supernatant) in order to evaluate the abundance and pattern of expression of the polymorphic protein. Anti-polymorphic antibodies can be used diagnostically to monitor protein levels in tissue as part of a clinical testing procedure, *e.g.*, to, for example, determine the efficacy of a given treatment regimen. Detection can be facilitated by coupling (*i.e.*, physically linking) the antibody to a detectable substance. Examples of detectable substances include various enzymes, prosthetic groups, fluorescent materials, luminescent materials, bioluminescent materials, and radioactive materials. Examples of suitable enzymes include horseradish peroxidase, alkaline phosphatase, -g a lactosidase, or acetylcholinesterase; examples of suitable prosthetic group complexes include streptavidin/biotin and avidin/biotin; examples of suitable fluorescent materials include umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or phycoerythrin; an example of a luminescent material includes luminol; examples of bioluminescent materials include luciferase, luciferin, and aequorin, and examples of suitable radioactive material include ^{125}I, ^{131}I, ^{35}S or ^{3}H.

EQUIVALENTS

From the foregoing detailed description of the specific embodiments of the invention, it should be apparent that unique compositions and methods of use thereof in SNPs in known genes have been described. Although particular embodiments have been disclosed herein in detail, this has been done by way of example for purposes of illustration only, and is not intended to be limiting with respect to the scope of the appended claims which follow. In particular, it is contemplated by the inventor that various substitutions, alterations, and modifications may be made to the invention without departing from the spirit and scope of the invention as defined by the claims.

Seq ID	CuraGen sequence ID	Base pos. of SNP	Polymorphic sequence	Base before	Base after	Amino acid before	Amino acid after	Type of change	Protein classification of CuraGen gene	Name of protein identified following a BLASTX analysis of the CuraGen sequence	Similiarity (pValue) following a BLASTX analysis	Map location
1	cg44131670	631	TTCTCGTTCCTGACAAGTGCAAATT[T/C]TTACACCAGGAGAGGATGGATGTTT	T	C	Phe	Phe	SILENT-CODING	amyloid	Human Gene SPTREMBL-ID:Q60496 PUTATIVE AMYLOID PRECURSOR PROTEIN - CAVIA PORCELLUS (GUINEA PIG), 695 aa.	0	21
2	cg44131386	1635	AAACATCCATCCTCTCCTGGTGTAA[A/G]AATTTGCACTTGTCAGGAACGAGAA	A	G	Phe	Phe	SILENT-CODING	amyloid	Human Gene SPTREMBL-ID:Q13764 AMYLOID-BETA PROTEIN - HOMO SAPIENS (HUMAN), 547 aa.	1.20E-304	
3	cg43323142	246	GGCAGCCCCATGGTGGTGGCTGGGG[A/G]CAGCCTCATGGTGGTGGCTGGGGGC	A	G	Gly	Gly	SILENT-CODING	amyloid	Human Gene Similar to SPTREMBL-ID:Q16409 PRP AMYLOID - HOMO SAPIENS (HUMAN), 97 aa (fragment).	4.20E-55	20 (20pter)
4	cg43323142	342	GGCAGCCTCATGGTGGTGGCTGGGG[A/G]CAGCCCATGGTGGTGGCTGGGGGC	A	G	Gly	Gly	SILENT-CODING	amyloid	Human Gene Similar to SPTREMBL-ID:Q16409 PRP AMYLOID - HOMO SAPIENS (HUMAN), 97 aa (fragment).	4.20E-55	20 (20pter)
5	cg43921977	2720	TATTATCCAATGTTAAGAGAGTATG[A/G]AAATTATTCATCCAAGTTTCCATAT	A	G	Phe	Phe	SILENT-CODING	apoptosis	Human Gene SWISSPROT-ID:P55060 CELLULAR APOPTOSIS SUSCEPTIBILITY PROTEIN - HOMO SAPIENS (HUMAN), 971 aa.	0.00E+00	20
6	cg43948568	2108	TCATATGGGGCCTGAACAGCTCGCG[A/G]CTCAGCAGGACGTCCCAGAGCTGGT	A	G	Ser	Ser	SILENT-CODING	apoptosis	Human Gene SWISSPROT-ID:P55211 CASPASE-9 PRECURSOR (EC 3.4.22.-) (CASP-9) (ICE-LIKE APOPTOTIC PROTEASE 6) (ICE-LAP6) (APOPTOTIC PROTEASE MCH-6) (APOPTOTIC PROTEASE ACTIVATING FACTOR 3) (APAF-3) - HOMO SAPIENS (HUMAN), 416 aa.	2.00E-222	1

7	cg44001801	1601	AGGAGCCTCTTC CTGGGCTCCTCC A[C/T]GAGTAATA GCCTGGAACCGT GGAAT	C	T	Ser	Ser	SILENT-CODING	apoptosis	Human Gene SWISSPROT-ID:P55210 CASPASE-7 PRECURSOR (EC 3.4.22.-) (ICE-LIKE APOPTOTIC PROTEASE 3) (ICE-LAP3) (APOPTOTIC PROTEASE MCH-3) (CMH-1) - HOMO SAPIENS (HUMAN), 303 aa.	6.00E-166	10
8	cg42913771	334	TACTGCTCAAAA TTCATGAGGTGT C[G/A]ACTTCCAG CCACGTAGATGC CGATT	G	A	Ser	Ser	SILENT-CODING	apoptosis	Human Gene Homologous to SWISSPROT-ID:P55212 CASPASE-6 PRECURSOR (EC 3.4.22.-) (APOPTOTIC PROTEASE MCH-2) - HOMO SAPIENS (HUMAN), 293 aa.	6.20E-116	
9	cg42913771	340	TCAAAATTCATG AGGTGTCGACTT C[C/T]AGCCACGT AGATGCCGATTG CTTCC	C	T	Ser	Ser	SILENT-CODING	apoptosis	Human Gene Homologous to SWISSPROT-ID:P55212 CASPASE-6 PRECURSOR (EC 3.4.22.-) (APOPTOTIC PROTEASE MCH-2) - HOMO SAPIENS (HUMAN), 293 aa.	6.20E-116	
10	cg42913771	364	CCAGCCACGTAG ATGCCGATTGCT T[C/T]CTGTGTGT CTTCCTGAGCCA CGGGG	C	T	Phe	Phe	SILENT-CODING	apoptosis	Human Gene Homologous to SWISSPROT-ID:P55212 CASPASE-6 PRECURSOR (EC 3.4.22.-) (APOPTOTIC PROTEASE MCH-2) - HOMO SAPIENS (HUMAN), 293 aa.	6.20E-116	
11	cg42913771	397	TCTTCCTGAGCC ACGGGGAAGGC AA[C/T]CACATTT ACGCATACGATG CCAAAA	C	T	Asn	Asn	SILENT-CODING	apoptosis	Human Gene Homologous to SWISSPROT-ID:P55212 CASPASE-6 PRECURSOR (EC 3.4.22.-) (APOPTOTIC PROTEASE MCH-2) - HOMO SAPIENS (HUMAN), 293 aa.	6.20E-116	
12	cg42913771	406	GCCACGGGGAA GGCAACCACATT TA[C/T]GCATACG ATGCCAAAATTG AAATTC	C	T	Tyr	Tyr	SILENT-CODING	apoptosis	Human Gene Homologous to SWISSPROT-ID:P55212 CASPASE-6 PRECURSOR (EC 3.4.22.-) (APOPTOTIC PROTEASE MCH-2) - HOMO SAPIENS (HUMAN), 293 aa.	6.20E-116	
13	cg42913771	412	GGGAAGGCAAC CACATTTACGCA TA[C/T]GATGCCA AAATTGAAATTC AGACCT	C	T	Tyr	Tyr	SILENT-CODING	apoptosis	Human Gene Homologous to SWISSPROT-ID:P55212 CASPASE-6 PRECURSOR (EC 3.4.22.-) (APOPTOTIC PROTEASE MCH-2) - HOMO SAPIENS (HUMAN), 293 aa.	6.20E-116	

14	cg42913771	418	GCAACCACATTTACGCATACGATGC[C/T]AAAATTGAAATTCAGACCTTGACTG	C	T	Ala	Ala	SILENT-CODING	apoptosis	Human Gene Homologous to SWISSPROT-ID:P55212 CASPASE-6 PRECURSOR (EC 3.4.22.-) (APOPTOTIC PROTEASE MCH-2) - HOMO SAPIENS (HUMAN), 293 aa.	6.20E-116	
15	cg42913771	424	ACATTTACGCATACGATGCCAAAAT[T/C]GAAATTCAGACCTTGACTGGCTTGT	T	C	Ile	Ile	SILENT-CODING	apoptosis	Human Gene Homologous to SWISSPROT-ID:P55212 CASPASE-6 PRECURSOR (EC 3.4.22.-) (APOPTOTIC PROTEASE MCH-2) - HOMO SAPIENS (HUMAN), 293 aa.	6.20E-116	
16	cg42913771	436	ACGATGCCAAAATTGAAATTCAGAC[C/A]TTGACTGGCTTGTTCAAAGGAGACA	C	A	Thr	Thr	SILENT-CODING	apoptosis	Human Gene Homologous to SWISSPROT-ID:P55212 CASPASE-6 PRECURSOR (EC 3.4.22.-) (APOPTOTIC PROTEASE MCH-2) - HOMO SAPIENS (HUMAN), 293 aa.	6.2E-116	
17	cg43271933	435	GGTTTGTGGAGTGCCAGGTCAGCCA[A/G]TGTGTCAGCAGTTCACCCTTCTACT	A	G	Gln	Gln	SILENT-CODING	apoptosis recep	Human Gene Homologous to SWISSPROT-ID:Q93038 WSL-1 PROTEIN PRECURSOR (APOPTOSIS-MEDIATING RECEPTOR DR3) (APOPTOSIS- MEDIATING RECEPTOR TRAMP) (DEATH DOMAIN RECEPTOR 3) (WSL PROTEIN) (APOPTOSIS INDUCING RECEPTOR AIR) (APO-3) (LYMPHOCYTE ASSOCIATED RECEPTOR QF DEATH) (LARD) - HOMO SAPIENS (HUMAN), 417 aa.	6.7E-103	1
18	cg43277632	3985	GTTTAACCATTTCTAGCGATGTCAG[T/C]GACGCTATGACAGACCACGAGATGA	T	C	Ser	Ser	SILENT-CODING	ATPase_associated	Human Gene SWISSPROT-ID:P35670 COPPER-TRANSPORTING ATPASE 2 (EC 3.6.1.36) (COPPER PUMP 2) (WILSON DISEASE-ASSOCIATED PROTEIN) - HOMO SAPIENS (HUMAN), 1465 aa.	0	13 (13q14.3)

19	cg43252813	1690	TCAGCCTTCATCGGAAATGCCGCTT[T/C]TGACTTCAACTAATGAATTTTATAC	T	C	Leu	Leu	SILENT-CODING	ATPase_associated	Human Gene SWISSNEW-ID:Q04656 COPPER-TRANSPORTING ATPASE 1 (EC 3.6.1.36) (COPPER PUMP 1) (MENKES DISEASE-ASSOCIATED PROTEIN) - HOMO SAPIENS (HUMAN), 1500 aa.\|pcls:SWISSPROT-ID:Q04656 COPPER-TRANSPORTING ATPASE 1 (EC 3.6.1.36) (COPPER PUMP 1) (MENKES DISEASE-ASSOCIATED PROTEIN) - HOMO SAPIENS (HUMAN), 1500 aa.	0	X (Xq12)
20	cg43939527	1245	AAGATGACCTCTCTGGTGCTGACAT[C/A]AAGGCAATCTGTACAGAAGCTGGTC	C	A	Ile	Ile	SILENT-CODING	ATPase_associated	Human Gene SWISSPROT-ID:P49014 26S PROTEASE REGULATORY SUBUNIT 4 (P26S4) - MUS MUSCULUS (MOUSE), AND RATTUS NORVEGICUS (RAT), 440 aa.	1.5E-233	14
21	cg43933946	961	ATATGTGGGTCCGACCCTCTAGATC[G/A]GGCAAGCTAAATTCAATTTTTCTAT	G	A	Pro	Pro	SILENT-CODING	ATPase_associated	Human Gene SWISSPROT-ID:P35998 26S PROTEASE REGULATORY SUBUNIT 7 (MSS1 PROTEIN) - HOMO SAPIENS (HUMAN), 433 aa.	5.2E-231	7
22	cg43933946	826	GTGCTCTGATGGCAAACATACCAGC[C/T]TCTGTGCAGACGCTTCTAATCTCAG	C	T	Glu	Glu	SILENT-CODING	ATPase_associated	Human Gene SWISSPROT-ID:P35998 26S PROTEASE REGULATORY SUBUNIT 7 (MSS1 PROTEIN) - HOMO SAPIENS (HUMAN), 433 aa.	5.20E-231	7
23	cg43933946	838	CAAACATACCAGCCTCTGTGCAGAC[G/A]CTTCTAATCTCAGCACCAGTGCTAT	G	A	Ser	Ser	SILENT-CODING	ATPase_associated	Human Gene SWISSPROT-ID:P35998 26S PROTEASE REGULATORY SUBUNIT 7 (MSS1 PROTEIN) - HOMO SAPIENS (HUMAN), 433 aa.	5.20E-231	7
24	cg43933946	937	TCATTGAACGAGCGTGAATCTTAAA[T/G]ATGTGGGTCCGACCCTCTAGATCGG	T	G	Ile	Ile	SILENT-CODING	ATPase_associated	Human Gene SWISSPROT-ID:P35998 26S PROTEASE REGULATORY SUBUNIT 7 (MSS1 PROTEIN) - HOMO SAPIENS (HUMAN), 433 aa.	5.20E-231	7

25	cg43916747	445	GCATCAAGGAG GAGACGGAGAT CCT[T/C]GAAGG GGAGGTGGTGG AGATCCAGA	T	C	Leu	Leu	SILENT-CODING	ATPase_ associated	Human Gene SPTREMBL-ID:Q12464 CHROMOSOME XVI READING FRAME ORF YPL235W - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 471 aa.	4.00E-163	19
26	cg43284434	2039	AGATGGGCCAC CTGACCTGCTTC GC[T/G]GGGGGC ATGTTCGCACTC GGGGCTG	T	G	Ala	Ala	SILENT-CODING	ATPase_ associated	Human Gene Homologous to SPTREMBL-ID:Q18788 C52E4.5 - CAENORHABDITIS ELEGANS, 590 aa.	4.00E-121	6
27	cg43251803	2941	TGAGGTAGCAG GACACTGCCATC TG[A/G]ATCTGCT CGGTACGCACTC GTTTCA	A	G	Ile	Ile	SILENT-CODING	ATPase_ associated	Human Gene Homologous to TREMBLNEW-ID:G1732075 TBP-ASSOCIATED FACTOR - HOMO SAPIENS (HUMAN), 801 aa (fragment).	3.10E-105	
28	cg43986887	320	CAAACTGCCTGT GATCCACTCGGT C[G/A]AGGAAGG CTTTCCGTTCAA TGTACC	G	A	Leu	Leu	SILENT-CODING	ATPase_ associated	Human Gene Similar to SPTREMBL-ID:O00393 P97 HOMOLOGOUS PROTEIN - HOMO SAPIENS (HUMAN), 277 aa (fragment).	7.90E-93	16
29	cg44022155	1125	TCCAGTACCTCA TCCTGGCTGCAG C[T/C]GTGTCCAA GGGGGCGCCCT TCCGCC	T	C	Ala	Ala	SILENT-CODING	ATPase_ associated	Human Gene Similar to SWISSPROT-ID:Q12697 PROBABLE CALCIUM-TRANSPORTING ATPASE 9 (EC 3.6.1.38) - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 1472 aa.	1.50E-63	1
30	cg44022155	903	GGCCAGCGCTG GTCCTGGGACG GGT[A/G]CGGCC ACCGGGGGCGC TGCTCAGCG	A	G	Val	Val	SILENT-CODING	ATPase_ associated	Human Gene Similar to SWISSPROT-ID:Q12697 PROBABLE CALCIUM-TRANSPORTING ATPASE 9 (EC 3.6.1.38) - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 1472 aa.	1.50E-63	1
31	cg43920913	364	GTGCAGATTTTG GAATGGCTGCTG A[T/C]AAGAATAA GTTTCCTGGAGA CAGCG	T	C	Asp	Asp	SILENT-CODING	biotindep	Human Gene SWISSPROT-ID:P05166 PROPIONYL-COA CARBOXYLASE BETA CHAIN PRECURSOR (EC 6.4.1.3) (PCCASE) (PROPANOYL-COA:CARBON DIOXIDE LIGASE) - HOMO SAPIENS (HUMAN), 539 aa.	8.20E-288	3 (3q21)

32	cg41562164	2748	GGCTGGCAATG CTCTCTCCAAAG TG[C/G]GCATTGT AGGCACCATCCC CAGTCA	C	G	Ala	Ala	SILENT-CODING	cadherin	Human Gene SWISSPROT-ID:Q13797 INTEGRIN ALPHA-9 PRECURSOR (INTEGRIN ALPHA-RLC) - HOMO SAPIENS (HUMAN), 1035 aa.\|pcls:SPTREMBL-ID:Q13797 INTEGRIN ALPHA SUBUNIT - HOMO SAPIENS (HUMAN), 1035 aa.	0.00E+00	3
33	cg43918042	3955	ACAGCCCAAGCA TGGGGCGATACA G[G/A]TCCGTTAA TGGTGGGCCCG GCAGTC	G	A	Arg	Arg	SILENT-CODING	cadherin	Human Gene TREMBLNEW-ID:G2852363 NF-PROTOCADHERIN - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 1035 aa.	0	4
34	cg42483174	1386	GTTAGAGTTAAA GCGGCTCCATAC N[T/G]GATCACAG CCCCTCAAAATC TTGTG	T	G	???	???	SILENT-CODING	cadherin	Human Gene SPTREMBL-ID:P97686 ANKYRIN BINDING CELL ADHESION MOLECULE NRCAM - RATTUS NORVEGICUS (RAT), 1215 aa (fragment).	0	7
35	cg43957225	2759	GGCCTTCCGGAT CAGCATTGCTGT T[C/T]CGGCAAG GAGAGAACTCG GCATAGG	C	T	Arg	Arg	SILENT-CODING	cadherin	Human Gene SWISSPROT-ID:P53708 INTEGRIN ALPHA-8 - HOMO SAPIENS (HUMAN), 1025 aa.	0.00E+00	10
36	cg43957225	2783	TCCGGCAAGGA GAGAACTCGGCA TA[G/A]GCGCTG AAGTTCTGAATT GCTACAT	G	A	Ala	Ala	SILENT-CODING	cadherin	Human Gene SWISSPROT-ID:P53708 INTEGRIN ALPHA-8 - HOMO SAPIENS (HUMAN), 1025 aa.	0.00E+00	10
37	cg43312078	1430	TCCTAGCGTGTA CCCCCTTGACCG G[T/C]TGGAGATT GAATTACTTAAG GGGGA	T	C	Leu	Leu	SILENT-CODING	cadherin	Human Gene SPTREMBL-ID:Q28260 VASCULAR CELL ADHESION MOLECULE-1 - CANIS FAMILIARIS (DOG), 739 aa.	0.00E+00	1 (1p32)
38	cg44026834	1209	CGGAGGTGAGG GTGGAGTAGTCC CT[G/C]GGCAGT GTGGTCGAGTGT GAGTGTT	G	C	Pro	Pro	SILENT-CODING	cadherin	Human Gene SWISSPROT-ID:P16144 INTEGRIN BETA-4 SUBUNIT PRECURSOR (GP150) (CD104) - HOMO SAPIENS (HUMAN), 1875 aa.	0.00E+00	17 (17q11)

39	cg44026834	1221	TGGAGTAGTCCC TGGGCAGTGTG GT[C/T]GAGTGTG AGTGTTCTGAGC GGGTCA	C	T	Ser	Ser	SILENT-CODING	cadherin	Human Gene SWISSPROT-ID:P16144 INTEGRIN BETA-4 SUBUNIT PRECURSOR (GP150) (CD104) - HOMO SAPIENS (HUMAN), 1875 aa.	0.00E+00	17 (17q11)
40	cg42558238	2054	AGAGTGCAACCC TGACCTGTGAGA G[C/T]GACGCCA ACCCTCCCGTCT CCCACT	C	T	Ser	Ser	SILENT-CODING	cadherin	Human Gene SWISSNEW-ID:Q01665 B-CELL RECEPTOR CD22-BETA PRECURSOR (LEU-14) (B-LYMPHOCYTE CELL ADHESION MOLECULE) (BL-CAM) - HOMO SAPIENS (HUMAN), 847 aa.\|pcls:SWISSPROT-ID:Q01665 B-CELL RECEPTOR CD22-BETA PRECURSOR (LEU-14) (B-LYMPHOCYTE CELL ADHESION MOLECULE) (BL-CAM) - HOMO SAPIENS (HUMAN), 847 aa.	0.00E+00	19 (19q13.1)
41	cg42558238	2225	AGGGCCGTTCG CCTCTCAGCACC CT[C/T]ACCGTCT ACTATAGCCCGG AGACCA	C	T	Leu	Leu	SILENT-CODING	cadherin	Human Gene SWISSNEW-ID:Q01665 B-CELL RECEPTOR CD22-BETA PRECURSOR (LEU-14) (B-LYMPHOCYTE CELL ADHESION MOLECULE) (BL-CAM) - HOMO SAPIENS (HUMAN), 847 aa.\|pcls:SWISSPROT-ID:Q01665 B-CELL RECEPTOR CD22-BETA PRECURSOR (LEU-14) (B-LYMPHOCYTE CELL ADHESION MOLECULE) (BL-CAM) - HOMO SAPIENS (HUMAN), 847 aa.	0	19 (19q13.1)

42	cg42558238	2228	GCCGTTCGCCTC TCAGCACCCTCA C[C/T]GTCTACTA TAGCCCGGAGA CCATCG	C	T	Thr	Thr	SILENT-CODING	cadherin	Human Gene SWISSNEW-ID:Q01665 B-CELL RECEPTOR CD22-BETA PRECURSOR (LEU-14) (B-LYMPHOCYTE CELL ADHESION MOLECULE) (BL-CAM) - HOMO SAPIENS (HUMAN), 847 aa. Ipcls:SWISSPROT-ID:Q01665 B-CELL RECEPTOR CD22-BETA PRECURSOR (LEU-14) (B-LYMPHOCYTE CELL ADHESION MOLECULE) (BL-CAM) - HOMO SAPIENS (HUMAN), 847 aa.	0	19 (19q13.1)	
43	cg44923512	657	AGGAAATGGACC CAGTGACTCAGC T[G/C]TATACCAT GAGTTGCACCCT GGAGT	G	C	Leu	Leu	SILENT-CODING	cadherin	Human Gene SWISSNEW-ID:Q13740 CD166 ANTIGEN PRECURSOR (ACTIVATED LEUKOCYTE-CELL ADHESION MOLECULE) (ALCAM) - HOMO SAPIENS (HUMAN), 583 aa. Ipcls:SWISSPROT-ID:Q13740 CD166 ANTIGEN PRECURSOR (ACTIVATED LEUKOCYTE-CELL ADHESION MOLECULE) (ALCAM) - HOMO SAPIENS (HUMAN), 583 aa.	1.7e-310	3 (3q13.1)	
44	cg43956560	1283	GGCTGGCAAGG AGATTAAAAAAA GG[C/T]AAGAAAT CCAAGAGAAGTA TGAATG	C	T	Gly	Gly	SILENT-CODING	cadherin	Human Gene SWISSPROT-ID:P14151 L-SELECTIN PRECURSOR (LYMPH NODE HOMING RECEPTOR) (LEUKOCYTE ADHESION MOLECULE-1) (LAM-1) (LEUKOCYTE SURFACE ANTIGEN LEU-8) (TQ1) (GP90-MEL) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 1) (LECAM1) (CD62L) - HOMO SAPIENS (HUMAN), 372 aa.	1E-218	1 (1q23)	

45	*cg43956560*	521	CGTGGGTGGGA ACCAACAAATCT CT[T/C]ACTGAAG AAGCAGAGAACT GGGGAG	T	C	Leu	Leu	SILENT-CODING	cadherin	Human Gene SWISSPROT-ID:P14151 L-SELECTIN PRECURSOR (LYMPH NODE HOMING RECEPTOR) (LEUKOCYTE ADHESION MOLECULE-1) (LAM-1) (LEUKOCYTE SURFACE ANTIGEN LEU-8) (TQ1) (GP90-MEL) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 1) (LECAM1) (CD62L) - HOMO SAPIENS (HUMAN), 372 aa.	1E-218	1 (1q23)
46	cg43977366	1646	CCTGGAAAGAAA TTCTGAACCTCC T[G/C]TACAAATT GCTGGCTGCTCT CATTC	G	C	Leu	Leu	SILENT-CODING	calcium_ channel	Human Gene TREMBLNEW-ID:G259184 RYANODINE RECEPTOR/CALCIUM RELEASE CHANNEL - ORYCTOLAGUS SP, 4872 aa.	0	15
47	cg43280376	1374	CCTGGGACATGA TGGTGCACTCCC G[C/T]TCCCACCA GCACGTGAAGAT CACCT	C	T	Arg	Arg	SILENT-CODING	carboxyla se	Human Gene SWISSPROT-ID:P38435 VITAMIN K-DEPENDENT GAMMA-CARBOXYLASE (EC 6.4.-.-) (GAMMA-GLUTAMYL CARBOXYLASE) - HOMO SAPIENS (HUMAN), 758 aa.	0	2
48	cg43307396	285	TTGTCCAGGGAA GCCTGGACAGC CT[G/A]CCCCAG GCAGTGAGGGA GTTTCTCG	G	A	Leu	Leu	SILENT-CODING	carboxyla se	Human Gene SWISSPROT-ID:P35558 PHOSPHOENOLPYRUVATE CARBOXYKINASE, CYTOSOLIC (GTP) (EC 4.1.1.32) (PHOSPHOENOLPYRUVATE CARBOXYLASE) (PEPCK-C) - HOMO SAPIENS (HUMAN), 622 aa.	0	20 (20q13.3 1)
49	cg43919581	709	AGCCCTACAGCG GGCGGAGGCCA GA[T/C]GCCATCA GGCTGGGCCTG GGGAACC	T	C	Asp	Asp	SILENT-CODING	cathepsin	Human Gene SWISSPROT-ID:P00750 TISSUE PLASMINOGEN ACTIVATOR PRECURSOR (EC 3.4.21.68) (TPA) (T-PLASMINOGEN ACTIVATOR) - HOMO SAPIENS (HUMAN), 562 aa.	0	8 (8p12)
50	cg42094324	835	CTGGGGGTCCA CTTGTCTGTAAT GG[T/G]GTGCTT CAAGGTATCACA TCATGGG	T	G	Gly	Gly	SILENT-CODING	cathepsin	Human Gene Homologous to SWISSPROT-ID:P20151 GLANDULAR KALLIKREIN 2 PRECURSOR (EC 3.4.21.35) (TISSUE KALLIKREIN) (PROSTATE) (HGK-1) - HOMO SAPIENS (HUMAN), 261 aa.	2.1E-147	19 (19q13.2)

51	cg43980411	1251	GCCCACAGTTTG TGGCAGATCATC C[T/G]TTTCTTTT TCTTATTATGCAT AAGA	T	G	Pro	Pro	SILENT-CODING	cathepsin inhib	Human Gene SWISSPROT-ID:P05120 PLASMINOGEN ACTIVATOR INHIBITOR-2, PLACENTAL (PAI-2) (MONOCYTE ARG- SERPIN) (UROKINASE INHIBITOR) - HOMO SAPIENS (HUMAN), 415 aa.	3.2E-222	18 (18q21.3)
52	cg43266931	673	GCGTGTCCACC GTGGTGAGGGT GAA[A/G]GGTAC GCCCTTGAGGA GCAGGACCA	A	G	Pro	Pro	SILENT-CODING	chloride_ channel	Human Gene Similar to SWISSNEW-ID:O15247 CHLORIDE INTRACELLULAR CHANNEL PROTEIN 2 (XAP121) - HOMO SAPIENS (HUMAN), 243 aa.\|pcls:SWISSPROT-ID:O15247 CHLORIDE INTRACELLULAR CHANNEL PROTEIN 2 (XAP121) - HOMO SAPIENS (HUMAN), 243 aa.	3.1E-59	9
53	cg43970982	2113	AGGAGAACAAG GCATTTCTGGAC CT[C/A]GGGGAA GCGGAGGTGCC GCTGGTGC	C	A	Arg	Arg	SILENT-CODING	collagen	Human Gene SWISSPROT-ID:P12111 COLLAGEN ALPHA 3(VI) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 3176 aa.	0	2
54	cg43970982	2136	CTCGGGGAAGC GGAGGTGCCGC TGG[T/C]GCTCCT GGAGAACGAGG CAGAACCG	T	C	Gly	Gly	SILENT-CODING	collagen	Human Gene SWISSPROT-ID:P12111 COLLAGEN ALPHA 3(VI) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 3176 aa.	0	2
55	cg43970982	2307	GAGGCAAAAAAG GAGAAAGAGGAT T[C/T]CCTGGATA CCCAGGACCAAA GGGTA	C	T	Phe	Phe	SILENT-CODING	collagen	Human Gene SWISSPROT-ID:P12111 COLLAGEN ALPHA 3(VI) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 3176 aa.	0	2
56	cg43970982	2460	CTGGCTACCCAG GACCAGCTGGTC C[C/A]AAGGGCA ACAGGGGCGAC TCCATCG	C	A	Pro	Pro	SILENT-CODING	collagen	Human Gene SWISSPROT-ID:P12111 COLLAGEN ALPHA 3(VI) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 3176 aa.	0	2

57	cg43131198	5627	GCCGGCAGGGA ACTTGCCACTTT TT[C/T]GCAAATA AGTATAGCTTCT GGCTCA	C	T	Phe	Phe	SILENT-CODING	collagen	Human Gene SWISSPROT-ID:P53420 COLLAGEN ALPHA 4(IV) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 1690 aa.	0	2 (2q36)
58	cg43970983	2931	GCGTGAGGCTG AGTGTCCTAGGG CC[G/A]GCTGGA GAAGGGCCCTCT GCAGAGG	G	A	Pro	Pro	SILENT-CODING	collagen	Human Gene SWISSPROT-ID:Q02388 COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR (LONG-CHAIN COLLAGEN) (LC COLLAGEN) - HOMO SAPIENS (HUMAN), 2944 aa.	0	3 (3p21.3)
59	cg43970983	9092	GTCCGTTATTTC AGTGACTTGGTC C[C/A]GTGGGTC TAGCCTTCCCCC CTGTGG	C	A	Pro	Pro	SILENT-CODING	collagen	Human Gene SWISSPROT-ID:Q02388 COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR (LONG-CHAIN COLLAGEN) (LC COLLAGEN) - HOMO SAPIENS (HUMAN), 2944 aa.	0	3 (3p21.3)
60	cg40339378	4366	TACCTGGCATCC CCGGTAAAGATG G[C/T]CCCAGTG GGCTCCCAGGC CCACCTG	C	T	Gly	Gly	SILENT-CODING	collagen	Human Gene SPTREMBL-ID:Q12823 A TYPE IV COLLAGEN - HOMO SAPIENS (HUMAN), 1690 aa (fragment).	0	X (Xq22)
61	cg43011543	391	CGCCAAGAATGG GCAAGGAAGCC GT[A/T]CCCAAGA AAGGCAAAGAAA TACCAT	A	T	Val	Val	SILENT-CODING	collagen	Human Gene SWISSPROT-ID:P27658 COLLAGEN ALPHA 1(VIII) CHAIN PRECURSOR (ENDOTHELIAL COLLAGEN) - HOMO SAPIENS (HUMAN), 744 aa.	0	
62	cg43991318	3003	CTTCGGGGCCCT GCTCTCCTTTGG G[G/C]CCGGGCT GCCCAGGCCGT CCTGCCA	G	C	Gly	Gly	SILENT-CODING	collagen	Human Gene Similar to SWISSPROT-ID:Q07092 COLLAGEN ALPHA 1(XVI) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 1603 aa.	1.3E-73	1 (1p34)
63	cg43281450	1145	CCATCTTGGCTT TTTGCCCTCCGA T[G/T]ATGCGCTG CCTCTGTTCCAC GGGGT	G	T	Ile	Ile	SILENT-CODING	complement	Human Gene SWISSPROT-ID:P00736 COMPLEMENT C1R COMPONENT PRECURSOR (EC 3.4.21.41) - HOMO SAPIENS (HUMAN), 705 aa.	0	12 (12p13)

64	cg43084083	4497	TTCTCAGTCCTG CCACTTTCACAG T[G/T]TACGAATA CCACAGACCAGA TAAAC	G	T	Val	Val	SILENT-CODING	complement	Human Gene SWISSPROT-ID:P01031 COMPLEMENT C5 PRECURSOR (CONTAINS: C5A ANAPHYLATOXIN) - HOMO SAPIENS (HUMAN), 1676 aa.	0	9 (9q34.1)
65	cg43029279	578	AACCAGGATATG CAACAGCAGATG G[G/A]AATTCTTC AGGATCAATTAC ATGTT	G	A	Gly	Gly	SILENT-CODING	complement	Human Gene SWISSPROT-ID:Q02985 COMPLEMENT FACTOR H-LIKE PROTEIN DOWN16 PRECURSOR - HOMO SAPIENS (HUMAN), 331 aa.	7.5E-191	
66	cg43029279	659	GCATTAATTCTT CAGAAAAGTGTG G[G/A]CCTCCTC CACCTATTAGCA ATGGTG	G	A	Gly	Gly	SILENT-CODING	complement	Human Gene SWISSPROT-ID:Q02985 COMPLEMENT FACTOR H-LIKE PROTEIN DOWN16 PRECURSOR - HOMO SAPIENS (HUMAN), 331 aa.	7.5E-191	
67	cg43956185	890	TAGAATCTTTGC ATTGAGGTGGTT C[C/T]GTCCAGTT TCCATTTAAACA CATCA	C	T	Thr	Thr	SILENT-CODING	complement	Human Gene SWISSPROT-ID:Q03591 COMPLEMENT FACTOR H-LIKE PROTEIN 1 PRECURSOR (H36) - HOMO SAPIENS (HUMAN), 330 aa.	4.1E-190	1
68	cg43956185	536	CCAGTTTCCCAT CCCAACATGTTG T[A/T]CGCAATGT GTGAGAACGTGA TGAAA	A	T	Arg	Arg	SILENT-CODING	complement	Human Gene SWISSPROT-ID:Q03591 COMPLEMENT FACTOR H-LIKE PROTEIN 1 PRECURSOR (H36) - HOMO SAPIENS (HUMAN), 330 aa.	4.10E-190	1
69	cg43956185	572	GAGAACGTGATG AAAGACGATATC C[A/C]CGTTTACA CACAAATTCAGC TGATT	A	C	Arg	Arg	SILENT-CODING	complement	Human Gene SWISSPROT-ID:Q03591 COMPLEMENT FACTOR H-LIKE PROTEIN 1 PRECURSOR (H36) - HOMO SAPIENS (HUMAN), 330 aa.	4.10E-190	1
70	cg43956185	809	ATGAAGCTGGAG CATATACTGACA A[C/T]GGGAATGA AGTAATGTCCCC ATTGT	C	T	Pro	Pro	SILENT-CODING	complement	Human Gene SWISSPROT-ID:Q03591 COMPLEMENT FACTOR H-LIKE PROTEIN 1 PRECURSOR (H36) - HOMO SAPIENS (HUMAN), 330 aa.	4.10E-190	1

71	cg43956183	345	AGTAATGCCATT GATTCTATTTTTC [T/C]TCACAACTG GGATATACCAGT TTCC	T	C	Glu	Glu	SILENT-CODING	complement	Human Gene SWISSPROT-ID:P36980 COMPLEMENT FACTOR H-LIKE PROTEIN DDESK59 PRECURSOR - HOMO SAPIENS (HUMAN), 270 aa.	9.20E-154	1
72	cg21644442	1753	TGGAGCAACCAG AGGGCAGCCCC CT[G/C]ACTCAG GATGACAGACAG GTGGAAC	G	C	Leu	Leu	SILENT-CODING	csf	Human Gene SWISSPROT-ID:P09603 MACROPHAGE COLONY STIMULATING FACTOR-1 PRECURSOR (CSF-1) (MCSF) - HOMO SAPIENS (HUMAN), 554 aa.	5.00E-304	1 (1p21)
73	cg42542496	942	CAAACTTCACTG CCTCAGCCAGAA C[T/A]ACTGGCTC TGGGCTTCTGAA GTGGC	T	A	Thr	Thr	SILENT-CODING	csf	Human Gene SWISSPROT-ID:P40225 THROMBOPOIETIN PRECURSOR (MEGAKARYOCYTE COLONY STIMULATING FACTOR) (C-MPL LIGAND) (ML) (MEGAKARYOCYTE GROWTH AND DEVELOPMENT FACTOR) (MGDF) - HOMO SAPIENS (HUMAN), 353 aa.	1.20E-189	3 (3q26.3)
74	cg43931046	2043	AACAGATTATTG TTCATGCTTTATC [G/C]CCAGAACAT TTGTTGAACACA AGTG	G	C	Ser	Ser	SILENT-CODING	cyclin	Human Gene SPTREMBL-ID:P70413 CYCLIN D-INTERACTING MYB-LIKE PROTEIN - MUS MUSCULUS (MOUSE), 761 aa.	0:00E+00	7
75	cg43927697	992	TAGTTAGTTCCA TCAGGTATTTGG C[C/T]AAAGTATG TTGCTCGACATC AACCT	C	T	Leu	Leu	SILENT-CODING	cyclin	Human Gene SWISSPROT-ID:P14635 G2/MITOTIC-SPECIFIC CYCLIN B1 - HOMO SAPIENS (HUMAN), 433 aa.	3.60E-230	5 (5q12)
76	cg43926592	1705	AGAAGGTGCACT CTTGATCACTGG G[T/A]GGGGAGC TGCTGAGACTCT CCTCTC	T	A	Pro	Pro	SILENT-CODING	cyclin	Human Gene SPTREMBL-ID:Q16589 CYCLIN G2 - HOMO SAPIENS (HUMAN), 344 aa.	8.50E-183	4
77	cg43957094	2212	GCTTGCCCTGAT AAAAAAGCACCA G[C/G]CGGCGGA GCGGCCGCGGA GCGACCA	C	G	Arg	Arg	SILENT-CODING	cyclin	Human Gene SWISSPROT-ID:P24863 G1/S-SPECIFIC CYCLIN C - HOMO SAPIENS (HUMAN), 303 aa.	7.90E-164	6

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78	cg43242733	222	CTGCAGTCTCTG TCAAGATGATAG A[A/G]GTACTGAC AACAACTGACTC TCAGA	A	G	Glu	Glu	SILENT-CODING	cyclin	Human Gene SWISSPROT-ID:P51959 G2/MITOTIC-SPECIFIC CYCLIN G1 - HOMO SAPIENS (HUMAN), 295 aa.	1.30E-154	5
79	cg43996855	3862	TGGTCAGGTCCT TGTTGATGAGGC C[G/A]TCCTTGTC CAAGAATCGAGC TGGAT	G	A	Asp	Asp	SILENT-CODING	cyto450	Human Gene SPTREMBL-ID:Q93089 DIOXIN-INDUCIBLE CYTOCHROME P450 (EC 1.14.14.1) - HOMO SAPIENS (HUMAN), 543 aa.	3.20E-293	2 (2p22)
80	cg40333008	1612	CTGTAGTCTTGG TGCCCATACGAA C[C/A]GAATAGAT GGGGCCATATTT TTTCT	C	A	Ser	Ser	SILENT-CODING	cyto450	Human Gene SWISSNEW-ID:P05093 CYTOCHROME P450 XVIIA1 (P450-C17) (EC 1.14.99.9) (STEROID 17-ALPHA- HYDROXYLASE/17,20 LYASE) - HOMO SAPIENS (HUMAN), 508 aa.\|pcls:SWISSPROT-ID:P05093 CYTOCHROME P450 XVIIA1 (P450-C17) (EC 1.14.99.9) (STEROID 17-ALPHA- HYDROXYLASE/17,20 LYASE) - HOMO SAPIENS (HUMAN), 508 aa.	4.90E-274	10 (10q24.3)
81	cg40333008	1669	TGAAGAAGTTGT TATGCATATGGC C[A/G]TGTCTGG GGAGGAATGGC AGGCTGC	A	G	His	His	SILENT-CODING	cyto450	Human Gene SWISSNEW-ID:P05093 CYTOCHROME P450 XVIIA1 (P450-C17) (EC 1.14.99.9) (STEROID 17-ALPHA- HYDROXYLASE/17,20 LYASE) - HOMO SAPIENS (HUMAN), 508 aa.\|pcls:SWISSPROT-ID:P05093 CYTOCHROME P450 XVIIA1 (P450-C17) (EC 1.14.99.9) (STEROID 17-ALPHA- HYDROXYLASE/17,20 LYASE) - HOMO SAPIENS (HUMAN), 508 aa.	4.90E-274	10 (10q24.3)
82	cg43966704	1243	ACTTGAGGCCAG TGGGGAAGCCA GC[G/A]CCTCCA CGGCCCCTCAAA CCCGATG	G	A	Gly	Gly	SILENT-CODING	cytochro me	Human Gene SPTREMBL-ID:Q43840 NADH DEHYDROGENASE (EC 1.6.99.3) (CYTOCHROME C REDUCTASE) (TYPE I DEHYDROGENASE) - SOLANUM TUBEROSUM (POTATO), 487 aa.	5.80E-184	11

83	cg43966704	1279	CCCTCAAACCCG ATGTCTTGATCT C[G/A]CCCAGGA TCCAGTCGGGC CCCTTCA	G	A	Gly	Gly	SILENT-CODING	cytochrome	Human Gene SPTREMBL-ID:Q43840 NADH DEHYDROGENASE (EC 1.6.99.3) (CYTOCHROME C REDUCTASE) (TYPE I DEHYDROGENASE) - SOLANUM TUBEROSUM (POTATO), 487 aa.	5.80E-184	11
84	cg43966704	1294	TCTTGATCTCGC CCAGGATCCAGT C[G/C]GGCCCCT TCAGCAGGATCT CCTTTG	G	C	Pro	Pro	SILENT-CODING	cytochrome	Human Gene SPTREMBL-ID:Q43840 NADH DEHYDROGENASE (EC 1.6.99.3) (CYTOCHROME C REDUCTASE) (TYPE I DEHYDROGENASE) - SOLANUM TUBEROSUM (POTATO), 487 aa.	5.80E-184	11
85	cg43966704	1375	CTTTCAGCCTCC AGTCATGGCGG CC[G/A]TACAGGT TGGTGAAAATCC GGTCTT	G	A	Tyr	Tyr	SILENT-CODING	cytochrome	Human Gene SPTREMBL-ID:Q43840 NADH DEHYDROGENASE (EC 1.6.99.3) (CYTOCHROME C REDUCTASE) (TYPE I DEHYDROGENASE) - SOLANUM TUBEROSUM (POTATO), 487 aa.	5.80E-184	11
86	cg43962888	563	CCTCCATCTCCA ACAAGAGAATAG T[A/G]GGCTGCAT CTGTGAAGAGGA CAATA	A	G	Val	Val	SILENT-CODING	cytochrome	Human Gene Similar to SWISSPROT-ID:P10606 CYTOCHROME C OXIDASE POLYPEPTIDE VB PRECURSOR (EC 1.9.3.1) - HOMO SAPIENS (HUMAN), 129 aa.	5.10E-66	2 (2cen)
87	cg43962888	620	TCGTCTGGTTTT GGCTGCACAAAG G[C/G]GAGGCCC AGCGATGCCCC CGCTGTG	C	G	Gly	Gly	SILENT-CODING	cytochrome	Human Gene Similar to SWISSPROT-ID:P10606 CYTOCHROME C OXIDASE POLYPEPTIDE VB PRECURSOR (EC 1.9.3.1) - HOMO SAPIENS (HUMAN), 129 aa.	5.10E-66	2 (2cen)
88	cg39454979	2375	ACTTACTACGCT CCAAGATTACCA A[A/G]CCCAACGT GTACCATGAGTC CAAGC	A	G	Lys	Lys	SILENT-CODING	deaminase	Human Gene SWISSPROT-ID:P51400 DOUBLE-STRANDED RNA-SPECIFIC EDITASE 1 (EC 3.5.-.-) (DSRNA ADENOSINE DEAMINASE) (RNA EDITING ENZYME 1) - RATTUS NORVEGICUS (RAT), 711 aa.	0.00E+00	21
89	cg43275625	1124	GCTTGGACTCAT GGTACACGTTGG G[T/C]TTGGTAAT CTTGGAGCGTAG TAAGT	T	C	Lys	Lys	SILENT-CODING	deaminase	Human Gene SPTREMBL-ID:O00465 DSRNA ADENOSINE DEAMINASE DRADA2C - HOMO SAPIENS (HUMAN), 714 aa.	0.00E+00	21

90	cg42476357	891	ACCGGCGCCTG AAGTTCCTCTCC TC[G/C]AAGTTCC AGGTCCATCAGA TGCTTA	G	C	Ser	Ser	SILENT-CODING	deaminase	Human Gene SWISSPROT-ID:P23109 AMP DEAMINASE 1 (EC 3.5.4.6) (MYOADENYLATE DEAMINASE) (AMP DEAMINASE ISOFORM M) - HOMO SAPIENS (HUMAN), 747 aa.	0.00E+00	1 (1p21)
91	cg39454981	2495	ACTTACTACGCT CCAAGATTACCA A[A/G]CCCAACGT GTACCATGAGTC CAAGC	A	G	Lys	Lys	SILENT-CODING	deaminase	Human Gene SWISSPROT-ID:P78563 DOUBLE-STRANDED RNA-SPECIFIC EDITASE 1 (EC 3.5.-.-) (DSRNA ADENOSINE DEAMINASE) (RNA EDITING ENZYME 1) - HOMO SAPIENS (HUMAN), 741 aa.	0.00E+00	
92	cg41626024	635	TTGGGCCTGAG GACCTGCAGAAG AC[T/C]CAGTGAC AGCCAGAGAATG CCCACT	T	C	Thr	Thr	SILENT-CODING	deaminase	Human Gene Similar to SWISSPROT-ID:P32320 CYTIDINE DEAMINASE (EC 3.5.4.5) (CYTIDINE AMINOHYDROLASE) - HOMO SAPIENS (HUMAN), 146 aa.\|pcls:TREMBLNEW-ID:E1228801 CYTIDINE DEAMINASE (EC 3.5.4.5) - HOMO SAPIENS (HUMAN), 146 aa.	8.80E-78	1 (1p36.2)
93	cg34396112	3375	CAGTTCTCCTGG TGCCTCTGGACA C[A/T]AGTGTCAG CTTGGCCCCACT GGCCA	A	T	Leu	Leu	SILENT-CODING	dehydrogenase	Human Gene SPTREMBL-ID:Q16712 XANTHINE DEHYDROGENASE/OXIDASE (EC 1.1.1.204) - HOMO SAPIENS (HUMAN), 1333 aa.	0.00E+00	2 (2p23)
94	cg34396112	3660	TCAGCTCAGGGA TCCAGGCTGGG CA[G/A]ACAATCA TAGGAAACAGCA TATTCT	G	A	Val	Val	SILENT-CODING	dehydrogenase	Human Gene SPTREMBL-ID:Q16712 XANTHINE DEHYDROGENASE/OXIDASE (EC 1.1.1.204) - HOMO SAPIENS (HUMAN), 1333 aa.	0.00E+00	2 (2p23)
95	cg34396112	3870	TCAGCAACTCTG GGGGAAAAATG GG[C/T]TCCTGG GTTGGATCCAGG GGCGTGA	C	T	Glu	Glu	SILENT-CODING	dehydrogenase	Human Gene SPTREMBL-ID:Q16712 XANTHINE DEHYDROGENASE/OXIDASE (EC 1.1.1.204) - HOMO SAPIENS (HUMAN), 1333 aa.	0.00E+00	2 (2p23)
96	cg34396112	3876	ACTCTGGGGGAA AAATGGGCTCCT G[G/C]GTTGGAT CCAGGGGCGTG AACTCCT	G	C	Thr	Thr	SILENT-CODING	dehydrogenase	Human Gene SPTREMBL-ID:Q16712 XANTHINE DEHYDROGENASE/OXIDASE (EC 1.1.1.204) - HOMO SAPIENS (HUMAN), 1333 aa.	0.00E+00	2 (2p23)

97	cg34396112	4245	TTCCTATTCCTTC CACAGTTGTCAC[T/A]GCAACATGG TGCAAGGAGCA GATGG	T	A	Ala	Ala	SILENT-CODING	dehydrogenase	Human Gene SPTREMBL-ID:Q16712 XANTHINE DEHYDROGENASE/OXIDASE (EC 1.1.1.204) - HOMO SAPIENS (HUMAN), 1333 aa.	0.00E+00	2 (2p23)
98	cg34396112	4254	CTTCCACAGTTG TCACTGCAACAT G[G/A]TGCAAGG AGCAGATGGGG GCCAGGC	G	A	His	His	SILENT-CODING	dehydrogenase	Human Gene SPTREMBL-ID:Q16712 XANTHINE DEHYDROGENASE/OXIDASE (EC 1.1.1.204) - HOMO SAPIENS (HUMAN), 1333 aa.	0.00E+00	2 (2p23)
99	cg34396112	4362	TCACTGTGCAAG CCCCGCAGCCC CC[C/T]TCTCCAC AGCCGAGCTTG GTTCCAC	C	T	Glu	Glu	SILENT-CODING	dehydrogenase	Human Gene SPTREMBL-ID:Q16712 XANTHINE DEHYDROGENASE/OXIDASE (EC 1.1.1.204) - HOMO SAPIENS (HUMAN), 1333 aa.	0.00E+00	2 (2p23)
100	cg34396112	609	TCTCCGGGGTG GCAGGGCTGTCT AG[G/C]CGGAAG AGTTCCTTCACG TTATTAC	G	C	Arg	Arg	SILENT-CODING	dehydrogenase	Human Gene SPTREMBL-ID:Q16712 XANTHINE DEHYDROGENASE/OXIDASE (EC 1.1.1.204) - HOMO SAPIENS (HUMAN), 1333 aa.	0.00E+00	2 (2p23)
101	cg43314766	1860	CGGAAGCATCCA TAGTACGCCACG G[A/G]GATCCAAT CTGAAAAGCCTG TCTTG	A	G	Ser	Ser	SILENT-CODING	dehydrogenase	Human Gene SWISSPROT-ID:P00352 ALDEHYDE DEHYDROGENASE, CYTOSOLIC (EC 1.2.1.3) (CLASS 1) (ALHDII) (ALDH-E1) - HOMO SAPIENS (HUMAN), 500 aa.	7.20E-273	9 (9q21)
102	cg43996714	1683	TAGATTCAGTTA ATCTCTTGGCAA T[G/A]ACTCTTCG AATATTGCTGGC GGGGA	G	A	Val	Val	SILENT-CODING	dehydrogenase	Human Gene TREMBLNEW-ID:G2979625 PYRUVATE DEHYDROGENASE COMPLEX PROTEIN X SUBUNIT PRECURSOR - HOMO SAPIENS (HUMAN), 501 aa.	1.60E-266	11
103	cg43996714	2433	ATCTCCAATTAG CTCCGCGGCTTA C[A/G]GACCACC CAAGAGCCCCCT TCACCA	A	G	Ser	Ser	SILENT-CODING	dehydrogenase	Human Gene TREMBLNEW-ID:G2979625 PYRUVATE DEHYDROGENASE COMPLEX PROTEIN X SUBUNIT PRECURSOR - HOMO SAPIENS (HUMAN), 501 aa.	1.60E-266	11

104	cg43959104	779	ACAGGATCATTC TTCAGTAATATTC [A/T]GCCTTGACA AGCACAGCGGC TACAA	A	T	Ala	Ala	SILENT-CODING	dehydrogenase	Human Gene SWISSPROT-ID:P51648 FATTY ALDEHYDE DEHYDROGENASE (EC 1.2.1.3) (ALDEHYDE DEHYDROGENASE, MICROSOMAL) (CLASS 3) - HOMO SAPIENS (HUMAN), 485 aa.	1.30E-250	17 (17p11.2)
105	cg43259523	654	AGATGTGGATCA GCAGTGCTGAG CA[C/T]GCAGGG CTCTTTCTGGTG ATGGCAA	C	T	His	His	SILENT-CODING	dehydrogenase	Human Gene SWISSPROT-ID:P45954 ACYL-COA DEHYDROGENASE, SHORT/BRANCHED CHAIN SPECIFIC PRECURSOR (EC 1.3.99.-) (SBCAD) (2-METHYL BRANCHED CHAIN ACYL-COA DEHYDROGENASE) (2-MEBCAD) - HOMO SAPIENS (HUMAN), 432 aa.	2.00E-229	10 (10q25)
106	cg43057018	1242	TCAATCCTAGAG ACTTACATAAAC C[G/T]ATCCAGGA AGTTATCATTGA ATTGA	G	T	Pro	Pro	SILENT-CODING	dehydrogenase	Human Gene SWISSNEW-ID:P08319 ALCOHOL DEHYDROGENASE CLASS II PI CHAIN (EC 1.1.1.1) - HOMO SAPIENS (HUMAN), 391 aa.\|pcls:SWISSPROT-ID:P08319 ALCOHOL DEHYDROGENASE CLASS II PI CHAIN (EC 1.1.1.1) - HOMO SAPIENS (HUMAN), 391 aa.	1.30E-209	4 (4q22)
107	cg44917703	1198	AGAAGGTGATCA AAGTTGGCAAGG T[G/T]CGGACTC GAGACATGGGC GGCTACA	G	T	Val	Val	SILENT-CODING	dehydrogenase	Human Gene TREMBLNEW-ID:G2737886 NAD+-SPECIFIC ISOCITRATE DEHYDROGENASE BETA PRECURSOR - HOMO SAPIENS (HUMAN), 385 aa.	8.80E-205	13
108	cg44917703	1216	GCAAGGTGCGG ACTCGAGACATG GG[C/T]GGCTAC AGCACCACAACC GACTTCA	C	T	Gly	Gly	SILENT-CODING	dehydrogenase	Human Gene TREMBLNEW-ID:G2737886 NAD+-SPECIFIC ISOCITRATE DEHYDROGENASE BETA PRECURSOR - HOMO SAPIENS (HUMAN), 385 aa.	8.80E-205	13
109	cg44917703	1222	TGCGGACTCGA GACATGGGCGG CTA[C/T]AGCACC ACAACCGACTTC ATCAAGT	C	T	Tyr	Tyr	SILENT-CODING	dehydrogenase	Human Gene TREMBLNEW-ID:G2737886 NAD+-SPECIFIC ISOCITRATE DEHYDROGENASE BETA PRECURSOR - HOMO SAPIENS (HUMAN), 385 aa.	8.80E-205	13

110	cg44917703	1243	GCTACAGCACCA CAACCGACTTCA T[C/T]AAGTCTGT CATCGGTCACCT GCAGA	C	T	Ile	Ile	SILENT-CODING	dehydrogenase	Human Gene TREMBLNEW-ID:G2737886 NAD+-SPECIFIC ISOCITRATE DEHYDROGENASE BETA PRECURSOR - HOMO SAPIENS (HUMAN), 385 aa.	8.80E-205	13
111	cg3000385	566	TGGGCACTGCTG GAAAAGTTATTA A[A/G]TGCAAAGC AGCTGTGCTTTG GGAGC	A	G	Lys	Lys	SILENT-CODING	dehydrogenase	Human Gene SWISSPROT-ID:P40394 ALCOHOL DEHYDROGENASE CLASS IV MU/SIGMA CHAIN (EC 1.1.1.1) (RETINOL DEHYDROGENASE) (GASTRIC ALCOHOL DEHYDROGENASE) - HOMO SAPIENS (HUMAN), 374 aa.	4.40E-202	4 (4q23)
112	cg43923979	863	GAAAATCTTTTG ACTGAGCTTCCG G[A/G]GGAAATTC AAAAGGAACCCC ATACA	A	G	Pro	Pro	SILENT-CODING	dehydrogenase	Human Gene SWISSPROT-ID:P11177 PYRUVATE DEHYDROGENASE E1 COMPONENT, BETA SUBUNIT PRECURSOR (EC 1.2.4.1) (PDHE1-B) - HOMO SAPIENS (HUMAN), 359 aa.	4.00E-192	3 (3p13)
113	cg43948373	1642	CAAGTGGGGCT GAGATTGGAGGT GC[C/A]TTTGGAG GAGAAAAGCACA CTGGTG	C	A	Ala	Ala	SILENT-CODING	dehydrogenase	Human Gene SWISSPROT-ID:P46562 HYPOTHETICAL ALDEHYDE-DEHYDROGENASE LIKE PROTEIN F01F1.6 - CAENORHABDITIS ELEGANS, 514 aa.	2.80E-184	5
114	cg43948373	1678	AAAAGCACACTG GTGGTGGCAGG GA[G/A]TCTGGC AGTGATGCCTGG AAACAGT	G	A	Glu	Glu	SILENT-CODING	dehydrogenase	Human Gene SWISSPROT-ID:P46562 HYPOTHETICAL ALDEHYDE-DEHYDROGENASE LIKE PROTEIN F01F1.6 - CAENORHABDITIS ELEGANS, 514 aa.	2.80E-184	5
115	cg43948373	1741	CTACTTGTACTA TCAACTACAGTA A[A/G]GACCTTCC TCTGGCCCAAGG AATCA	A	G	Lys	Lys	SILENT-CODING	dehydrogenase	Human Gene SWISSPROT-ID:P46562 HYPOTHETICAL ALDEHYDE-DEHYDROGENASE LIKE PROTEIN F01F1.6 - CAENORHABDITIS ELEGANS, 514 aa.	2.80E-184	5

116	cg43960596	903	CCAACAGGGTG GTGTGGAGGCG GGA[A/G]GAGGC CACCCGCTGCA GGTCCTCGG	A	G	Ser	Ser	SILENT-CODING	dehydrogenase	Human Gene SWISSNEW-ID:Q92781 11 CIS RETINOL DEHYDROGENASE (EC 1.1.1.105) (11-CIS RDH) - HOMO SAPIENS (HUMAN), 318 aa.\|pcls:SWISSPROT-ID:Q92781 11-CIS RETINOL DEHYDROGENASE (EC 1.1.1.105) (11-CIS RDH) - HOMO SAPIENS (HUMAN), 318 aa.	4.40E-170	12
117	cg43969759	566	CGTCTCGGATGG TGCTGAGTGGTG G[G/A]TAGAGTCT CCCCTGGGACA GATGCT	G	A	Tyr	Tyr	SILENT-CODING	dehydrogenase	Human Gene Homologous to SPTREMBL-ID:Q16797 NADP-DEPENDENT MALIC ENZYME (EC 1.1.1.40) (MALATE DEHYDROGENASE (OXALOACETATE DECARBOXYLATING) (NADP+)) (PYRUVIC-MALIC CARBOXYLASE) - HOMO SAPIENS (HUMAN), 572 aa.	1.80E-109	11
118	cg43104003	710	ACCCAGCGCCTA TGCTGGCCCGG AC[G/A]TCACTGA TAGGTAAGATGA AGTCCC	G	A	Asp	Asp	SILENT-CODING	dehydrogenase	Human Gene Similar to SWISSNEW-ID:P11586 C-1-TETRAHYDROFOLATE SYNTHASE, CYTOPLASMIC (C1-THF SYNTHASE) (METHYLENETETRAHYDROFOLATE DEHYDROGENASE (EC 1.5.1.5) / METHENYLTETRAHYDROFOLATE CYCLOHYDROLASE (EC 3.5.4.9) / FORMYLTETRAHYDROFOLATE SYNTHETASE (EC 6.3.4.3)) - HOMO SAPIENS (HUMAN), 934 aa.\|pcls:SWISSPROT-ID:P11586 C-1-TETRAHYDROFOLATE SYNTHASE, CYTOPLASMIC (METHYLENETETRAHYDROFOLATE DEHYDROGENASE (EC 1.5.1.5) / METHENYLTETRAHYDROFOLATE CYCLOHYDROLASE (EC 3.5.4.9) / FORMYLTETRAHYDROFOLATE SYNTHETASE (EC 6.3.4.3)) (C1-THF SYNTHASE) - HOMO SAPIENS (HUMAN), 934 aa.	7.10E-92	6

119	cg42717491	384	CTGTCTCTTTGGACTGAACAAAAGA[G/A]CACTCGATGACTCCTTCCTTCCCAT	G	A	Cys	Cys	SILENT-CODING	dehydrogenase	Human Gene Similar to SWISSPROT-ID:P04636 MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR (EC 1.1.1.37) - RATTUS NORVEGICUS (RAT), 338 aa.	2.40E-52	
120	cg43248620	2294	TCTGTACCCTCACGTGCAGGCTCCG[C/T]GATGTTTTGCTGGAAAGCTGAGCAG	C	T	Ser	Ser	SILENT-CODING	dna_rna_bind	Human Gene SPTREMBL-ID:Q14550 ZINC-FINGER DNA-BINDING PROTEIN - HOMO SAPIENS (HUMAN), 1482 aa.	0.00E+00	1
121	cg43273880	4271	GCTGTGTGTCAGCAATGCAGGAATA[C/T]GAAGAGCAGCTGAAAGAAAATGCCA	C	T	Tyr	Tyr	SILENT-CODING	dna_rna_bind	Human Gene SWISSPROT-ID:O14647 CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 2 (CHD-2) - HOMO SAPIENS (HUMAN), 1739 aa.	0.00E+00	15
122	cg43273880	4952	CTAGAAAAGACAAAGAAGGGGACAA[A/G]GAAAGAAAGAAAGGAAAAGATAAGA	A	G	Lys	Lys	SILENT-CODING	dna_rna_bind	Human Gene SWISSPROT-ID:O14647 CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 2 (CHD-2) - HOMO SAPIENS (HUMAN), 1739 aa.	0.00E+00	15
123	cg42175288	1364	ACAGAAGTGGGGGTGGCTATGGTGG[A/G]GACAGAAGCAGCGGTGGTGGCTACA	A	G	Gly	Gly	SILENT-CODING	dna_rna_bind	Human Gene SPTREMBL-ID:Q92804 PUTATIVE RNA BINDING PROTEIN RBP56 - HOMO SAPIENS (HUMAN), 592 aa.	0.00E+00	17
124	cg43968816	2369	TCCCTTCCCCTCGGGAGTTGCTCCA[C/G]GTACGGATCTGACTTTTGTTGGTAA	C	G	Thr	Thr	SILENT-CODING	dna_rna_bind	Human Gene SWISSPROT-ID:P27694 REPLICATION PROTEIN A 70 KD DNA-BINDING SUBUNIT (RP-A) (RF-A) - (REPLICATION FACTOR-A PROTEIN 1) (SINGLE-STRANDED DNA-BINDING PROTEIN) - HOMO SAPIENS (HUMAN), 616 aa.	0.00E+00	17 (17p13.3)

125	cg44005808	3412	AGACCACCTCTC AGGCCCACTCG CT[G/C]CCTCTCT CGCCTGCCTCCA CAAGGC	G	C	Leu	Leu	SILENT-CODING	dna_rna_bind	Human Gene SWISSNEW-ID:P19838 NUCLEAR FACTOR NF-KAPPA-B P105 SUBUNIT (DNA-BINDING FACTOR KBF1) (EBP- 1) [CONTAINS: NUCLEAR FACTOR NF-KAPPA-B P50 SUBUNIT] - HOMO SAPIENS (HUMAN), 969 aa.	pcls:SWISSPROT-ID:P19838 NUCLEAR FACTOR NF-KAPPA-B P105 SUBUNIT (CONTAINS: NUCLEAR FACTOR NF- KAPPA-B P50 SUBUNIT) (DNA-BINDING FACTOR KBF1) (EBP-1) HOMO SAPIENS (HUMAN), 969 aa.	0.00E+00	
126	cg43276473	311	CATCTGCTCCCA CCGTAACTCTAG T[A/G]CAGCTGC CCAATGGGCAGA CAGTTC	A	G	Val	Val	SILENT-CODING	dna_rna_bind	Human Gene Homologous to SPTREMBL-ID:Q62347 TRANSCRIPTION FACTOR/DNA BINDING PROTEIN - MUS MUSCULUS (MOUSE), 287 aa.	5.30E-142	2	
127	cg44031583	307	CAAACCTGATTG TACATCAGAGAA C[C/T]CATACAGG AGAGAAACCCTA TGGTT	C	T	Thr	Thr	SILENT-CODING	dna_rna_bind	Human Gene Homologous to SPTREMBL-ID:Q61491 DNA-BINDING PROTEIN - MUS MUSCULUS (MOUSE), 546 aa.	7.10E-125	12	
128	cg43969880	580	AACGGATACACA CGGGAGAGAAG CC[C/T]TATCAGT GCAAGGAGTGT GGGAAAA	C	T	Pro	Pro	SILENT-CODING	dna_rna_bind	Human Gene Similar to SPTREMBL-ID:Q61491 DNA-BINDING PROTEIN - MUS MUSCULUS (MOUSE), 546 aa.	9.40E-58	10	
129	cg43946971	1334	TGGCCATGCACA AGCGCAGTGCC CA[T/C]GGCGAG CTGGAGGCCAC GGAGGAGA	T	C	His	His	SILENT-CODING	dna_rna_bind	Human Gene Similar to SPTREMBL-ID:Q61491 DNA-BINDING PROTEIN - MUS MUSCULUS (MOUSE), 546 aa.	4.90E-52	6 (6p21.3)	
130	cg43946971	1361	GCGAGCTGGAG GCCACGGAGGA GAG[T/C]GAGCA GGCCCTCTATGA GCAGCAGC	T	C	Ser	Ser	SILENT-CODING	dna_rna_bind	Human Gene Similar to SPTREMBL-ID:Q61491 DNA-BINDING PROTEIN - MUS MUSCULUS (MOUSE), 546 aa.	4.90E-52	6 (6p21.3)	

131	cg43949306	1784	TGGAGTCTGTCC TCGTCTTCTTCT C[A/G]GTCTCTGC GTAGGCCAGGT CGTCCT	A	G	Thr	Thr	SILENT-CODING	dynein	Human Gene SWISSPROT-ID:P38650 DYNEIN HEAVY CHAIN, CYTOSOLIC (DYHC) (MAP 1C) - RATTUS NORVEGICUS (RAT), 4644 aa.	0.00E+00	14
132	cg43958656	565	GAACCGGCATG GCCAAAGCCGC GGC[G/A]ATCGG CATCGACCTGGG CACCACCT	G	A	Ala	Ala	SILENT-CODING	eph	Human Gene SWISSPROT-ID:P08107 HEAT SHOCK 70 KD PROTEIN 1 (HSP70.1) (HSP70-1/HSP70-2) - HOMO SAPIENS (HUMAN), 641 aa.	0.00E+00	6
133	cg43958656	763	AGAACACCGTGT TTGACGCGAAGC G[G/C]CTGATCG GCCGCAAGTTCG GCGACC	G	C	Arg	Arg	SILENT-CODING	eph	Human Gene SWISSPROT-ID:P08107 HEAT SHOCK 70 KD PROTEIN 1 (HSP70.1) (HSP70-1/HSP70-2) - HOMO SAPIENS (HUMAN), 641 aa.	0.00E+00	6
134	cg43958656	769	CCGTGTTTGACG CGAAGCGGCTG AT[C/T]GGCCGC AAGTTCGGCGAC CCGGTGG	C	T	Ile	Ile	SILENT-CODING	eph	Human Gene SWISSPROT-ID:P08107 HEAT SHOCK 70 KD PROTEIN 1 (HSP70.1) (HSP70-1/HSP70-2) - HOMO SAPIENS (HUMAN), 641 aa.	0.00E+00	6
135	cg44017749	10249	CCATTAACCGAG CCCACAAGACCA C[A/G]GGCACCA ACAAAACGCTCC TCATCA	A	G	Thr	Thr	SILENT-CODING	eph	Human Gene SWISSPROT-ID:Q07954 LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 1 PRECURSOR (LRP) (ALPHA-2-MACROGLOBULIN RECEPTOR) (A2MR) (APOLIPOPROTEIN E RECEPTOR) (APOER) (CD91) - HOMO SAPIENS (HUMAN), 4544 aa.	0.00E+00	12
136	cg43982507	2646	CCAATAAATTCA CTGGATCAGAGC T[A/T]GCCACTCT AGTCAACAACCT GAATG	A	T	Leu	Leu	SILENT-CODING	eph	Human Gene SWISSPROT-ID:P98155 VERY LOW-DENSITY LIPOPROTEIN RECEPTOR PRECURSOR (VLDL RECEPTOR) - HOMO SAPIENS (HUMAN), 873 aa.	0.00E+00	9 (9p24)
137	cg43982507	636	CCATGGGCACGT CCGCGCTCTGG GC[G/C]CTCTGG CTGCTGCTCGCG CTGTGCT	G	C	Ala	Ala	SILENT-CODING	eph	Human Gene SWISSPROT-ID:P98155 VERY LOW-DENSITY LIPOPROTEIN RECEPTOR PRECURSOR (VLDL RECEPTOR) - HOMO SAPIENS (HUMAN), 873 aa.	0.00E+00	9 (9p24)

138	cg43953981	2111	CTTGAACAAGTT TAGCTCCAATGT T[C/T]TTGTATTT ATCTTTTAAGTCA ATTG	C	T	Lys	Lys	SILENT-CODING	eph	Human Gene SWISSPROT-ID:P10809 MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (P60 LYMPHOCYTE PROTEIN) (60 KD CHAPERONIN) (HEAT SHOCK PROTEIN 60) (HSP-60) (PROTEIN CPN60) (GROEL PROTEIN) (HUCHA60) - HOMO SAPIENS (HUMAN), 573 aa.	8.30E-295	9	
139	cg43945167	1149	AGAGCTTGTCCA GTTCTTCGCCGG A[A/G]AATTTCCC AGAGGTCTTCGC CTTGT	A	G	Phe	Phe	SILENT-CODING	eph	Human Gene SWISSPROT-ID:P30533 ALPHA-2-MACROGLOBULIN RECEPTOR-ASSOCIATED PROTEIN PRECURSOR (ALPHA-2-MRAP) (LOW DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN- ASSOCIATED PROTEIN 1) (RAP) - HOMO SAPIENS (HUMAN), 357 aa.	9.60E-191	4 (4p16.3)	
140	cg43918531	1596	GCAAAAAGCAAC AGATATCTCTTG C[A/C]ACACAAAT GGTTAGAATGAT TTTGA	A	C	Ala	Ala	SILENT-CODING	eph	Human Gene Homologous to SWISSNEW-ID:Q52500 THERMOSOME SUBUNIT (HEAT-SHOCK PROTEIN) - PYROCOCCUS KODAKARAENSIS, 546 aa.	pcls:SWISSPROT-ID:Q52500 THERMOSOME SUBUNIT (HEAT-SHOCK PROTEIN) - PYROCOCCUS SP. (STRAIN KOD1), 546 aa.	1.00E-104	5
141	cg43918531	1611	TATCTCTTGCAA CACAAATGGTTA G[A/G]ATGATTTT GAAGATTGATGA CATTC	A	G	Arg	Arg	SILENT-CODING	eph	Human Gene Homologous to SWISSNEW-ID:Q52500 THERMOSOME SUBUNIT (HEAT-SHOCK PROTEIN) - PYROCOCCUS KODAKARAENSIS, 546 aa.	pcls:SWISSPROT-ID:Q52500 THERMOSOME SUBUNIT (HEAT-SHOCK PROTEIN) - PYROCOCCUS SP. (STRAIN KOD1), 546 aa.	1.00E-104	5

142	cg43918531	1618	TGCAACACAAATGGTTAGAATGATT[T/C]TGAAGATTGATGACATTCGTAAGCC	T	C	Leu	Leu	SILENT-CODING	eph	Human Gene Homologous to SWISSNEW-ID:Q52500 THERMOSOME SUBUNIT (HEAT-SHOCK PROTEIN) - PYROCOCCUS KODAKARAENSIS, 546 aa.]pcls:SWISSPROT-ID:Q52500 THERMOSOME SUBUNIT (HEAT-SHOCK PROTEIN) - PYROCOCCUS SP. (STRAIN KOD1), 546 aa.	1.00E-104	5
143	cg43944783	1309	TGTTGTAGTCGCCCTTTTCAAAGTA[C/T]ACCGCTGCTTGATTGGTAATGTAAG	C	T	Val	Val	SILENT-CODING	eph	Human Gene Similar to SWISSPROT-ID:P15705 HEAT SHOCK PROTEIN STI1 - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 589 aa.	2.80E-74	11
144	cg42889246	592	TCATTCAGACCTTCGAAGGCTGGCT[A/G]CTGATAAAAGCACAACACGGAACCA	A	G	Leu	Leu	SILENT-CODING	eph	Human Gene Similar to SPTREMBL-ID:Q12988 HEAT SHOCK PROTEIN 27 - HOMO SAPIENS (HUMAN), 241 aa.	7.50E-73	
145	cg42889246	679	CCCGACAGTACAAACTACCAGATGG[T/C]GTGGAAATCAAAGATTTGTCTGCAG	T	C	Gly	Gly	SILENT-CODING	eph	Human Gene Similar to SPTREMBL-ID:Q12988 HEAT SHOCK PROTEIN 27 - HOMO SAPIENS (HUMAN), 241 aa.	7.50E-73	
146	cg43984905	2206	ACCTTGCCCTCATCCGCTTCTTGGT[G/A]GAAGATTATGATGCCTCCTCCAAGA	G	A	Val	Val	SILENT-CODING	esterase	Human Gene SWISSPROT-ID:P51178 1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC-III) - HOMO SAPIENS (HUMAN), 756 aa.	0.00E+00	3

147	cg43984905	2227	TGGTGGAAGATTATGATGCCTCCTC[C/T]AAGAATGACTTCATTGGCCAGAGTA	C	T	Ser	Ser	SILENT-CODING	esterase	Human Gene SWISSPROT-ID:P51178 1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC-III) - HOMO SAPIENS (HUMAN), 756 aa.	0.00E+00	3
148	cg43984905	2233	AAGATTATGATGCCTCCTCCAAGAA[T/C]GACTTCATTGGCCAGAGTACCATCC	T	C	Asn	Asn	SILENT-CODING	esterase	Human Gene SWISSPROT-ID:P51178 1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC-III) - HOMO SAPIENS (HUMAN), 756 aa.	0.00E+00	3
149	cg43984905	2239	ATGATGCCTCCTCCAAGAATGACTT[C/T]ATTGGCCAGAGTACCATCCCCTTGA	C	T	Phe	Phe	SILENT-CODING	esterase	Human Gene SWISSPROT-ID:P51178 1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC-III) - HOMO SAPIENS (HUMAN), 756 aa.	0.00E+00	3
150	cg43984905	2254	AGAATGACTTCATTGGCCAGAGTAC[C/T]ATCCCCTTGAACAGCCTCAAGCAAG	C	T	Thr	Thr	SILENT-CODING	esterase	Human Gene SWISSPROT-ID:P51178 1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC-III) - HOMO SAPIENS (HUMAN), 756 aa.	0.00E+00	3

151	cg44011461	2429	GGATGAGGGCA TAGATGCTGCTG AA[G/C]GTGAGG TTGTCAGTCAAG TAGTATT	G	C	Thr	Thr	SILENT-CODING	esterase	Human Gene SWISSPROT-ID:P16885 1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE GAMMA 2 (EC 3.1.4.11) (PLC-GAMMA-2) (PHOSPHOLIPASE C-GAMMA-2) (PLC-IV) - HOMO SAPIENS (HUMAN), 1252 aa.	0.00E+00	16 (16q24.1)
152	cg44011461	2432	TGAGGGCATAGA TGCTGCTGAAGG T[G/C]AGGTTGTC AGTCAAGTAGTA TTTCA	G	C	Leu	Leu	SILENT-CODING	esterase	Human Gene SWISSPROT-ID:P16885 1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE GAMMA 2 (EC 3.1.4.11) (PLC-GAMMA-2) (PHOSPHOLIPASE C-GAMMA-2) (PLC-IV) - HOMO SAPIENS (HUMAN), 1252 aa.	0.00E+00	16 (16q24.1)
153	cg44011461	2750	CATCACTGAAGG ACAGCTTGGCAT C[G/A]GCAATGG CGCAGTAGTGCC GAGTCC	G	A	Ala	Ala	SILENT-CODING	esterase	Human Gene SWISSPROT-ID:P16885 1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE GAMMA 2 (EC 3.1.4.11) (PLC-GAMMA-2) (PHOSPHOLIPASE C-GAMMA-2) (PLC-IV) - HOMO SAPIENS (HUMAN), 1252 aa.	0.00E+00	16 (16q24.1)
154	cg40343531	592	AGGATCACTTAC TCTCACTCCCCG C[C/T]GCGGGGG TGGTGCTCAGCT GCTTGG	C	T	Ala	Ala	SILENT-CODING	esterasei nhib	Human Gene SPTREMBL-ID:Q14432 CGMP-INHIBITED CAMP PHOSPHODIESTERASE - HOMO SAPIENS (HUMAN), 1141 aa.	0.00E+00	12
155	cg43937658	1406	CATCTGCTGGGG CCACCTTTGCTG C[G/A]TAACTCCA CATCTCAATCCG GTCAT	G	A	Tyr	Tyr	SILENT-CODING	fgfrecept or	Human Gene SPTREMBL-ID:Q13221 CYSTEINE-RICH FIBROBLAST GROWTH FACTOR RECEPTOR - HOMO SAPIENS (HUMAN), 1177 aa.	0.00E+00	16

156	cg43320667	1510	CAGGAACGCCA GCCCGGGCTGA GGC[C/G]GCCAC ATCAGCAATGGA CCTCTTGG	C	G	Ala	Ala	SILENT-CODING	gaba	Human Gene SWISSPROT-ID:P30531 SODIUM- AND CHLORIDE-DEPENDENT GABA TRANSPORTER 1 - HOMO SAPIENS (HUMAN), 599 aa.	0.00E+00	3 (3p25)
157	cg43320667	852	GCTCAGGACCAT TCTCTGGGCGAA C[G/A]ATGTCTTC GCTGGGCTGGA CCATGA	G	A	Ile	Ile	SILENT-CODING	gaba	Human Gene SWISSPROT-ID:P30531 SODIUM- AND CHLORIDE-DEPENDENT GABA TRANSPORTER 1 - HOMO SAPIENS (HUMAN), 599 aa.	0.00E+00	3 (3p25)
158	cg43320667	908	ATGCGCTGCTTC AGGGAGCCCTTT A[A/G]GGTGAGG AACATGTAGGCC ATGTAC	A	G	Leu	Leu	SILENT-CODING	gaba	Human Gene SWISSPROT-ID:P30531 SODIUM- AND CHLORIDE-DEPENDENT GABA TRANSPORTER 1 - HOMO SAPIENS (HUMAN), 599 aa.	0.00E+00	3 (3p25)
159	cg44131042	556	ATCTTTATTCCCA GATCTCCTCTGT[C/T]CCCATAGGT TACAGCCACCCC GCCC	C	T	Val	Val	SILENT-CODING	gaba	Human Gene SWISSPROT-ID:P80404 4-AMINOBUTYRATE AMINOTRANSFERASE, MITOCHONDRIAL PRECURSOR (EC 2.6.1.19) (GAMMA-AMINO-N-BUTYRATE TRANSAMINASE) (GABA TRANSAMINASE) (GABA AMINOTRANSFERASE) - HOMO SAPIENS (HUMAN), 500 aa.	4.20E-268	16
160	cg3001932	230	CAAAAACTAAAG GGATGTGGAGA GT[G/C]CGGAAA AGGGGCTACTTT GGGATTT	G	C	Val	Val	SILENT-CODING	gaba	Human Gene SWISSPROT-ID:P47870 GAMMA-AMINOBUTYRIC-ACID RECEPTOR BETA-2 SUBUNIT PRECURSOR (GABA(A) RECEPTOR) - HOMO SAPIENS (HUMAN), 474 aa.	1.90E-256	5 (5q34)
161	cg43299024	2993	TGGCTGTGGCC CTGACCAAGGGT GG[G/A]GAGGCC CGAGGGGAGCT GTTCTGGG	G	A	Gly	Gly	SILENT-CODING	glucoamylase	Human Gene TREMBLNEW-ID:G2826521 MALTASE-GLUCOAMYLASE (EC 3.2.1.20) - HOMO SAPIENS (HUMAN), 1857 aa.	7.40E-199	17 (17q25.2)

162	cg43992911	1660	GAAAAGAAGTTAAGATCTTGAAGGG[C/T]CTGAACCTGAAGGTGCAGAGTGGGC	C	T	Gly	Gly	SILENT-CODING	glycoprotein	Human Gene SWISSPROT-ID:P08183 MULTIDRUG RESISTANCE PROTEIN 1 (P-GLYCOPROTEIN 1) - HOMO SAPIENS (HUMAN), 1280 aa.	0.00E+00	7
163	cg43286488	1436	GGTCAGCTTCAGCCAGATAGCCACT[G/A]GGGTCATGGAGCTGGAGGGCAAAGG	G	A	Pro	Pro	SILENT-CODING	glycoprotein	Human Gene SWISSNEW-ID:P40967 MELANOCYTE PROTEIN PMEL 17 PRECURSOR (MELANOCYTE LINEAGE SPECIFIC ANTIGEN GP100) (MELANOMA-ASSOCIATED ME20 ANTIGEN) (ME20M/ME20S) (ME20-M/ME20-S) (95 KD MELANOCYTE-SPECIFIC SECRETED GLYCOPROTEIN) - HOMO SAPIENS (HUMAN), 661 aa.\|pcls:SWISSPROT-ID:P40967 MELANOCYTE PROTEIN PMEL 17 PRECURSOR (MELANOCYTE LINEAGE-SPECIFIC ANTIGEN GP100) (MELANOMA-ASSOCIATED ME20 ANTIGEN) (ME20M) (ME20-M / ME20-S) (95 KD MELANOCYTE-SPECIFIC SECRETED GLYCOPROTEIN) - HOMO SAPIENS (HUMAN), 661 aa.	0.00E+00	12

164	cg43286488	1706	GGCCCCCTAGAACTTGCCAGTATTG[G/A]CCCCAGGTCTTCCAGACATAAACAA	G	A	Gly	Gly	SILENT-CODING	glycoprotein	Human Gene SWISSNEW-ID:P40967 MELANOCYTE PROTEIN PMEL 17 PRECURSOR (MELANOCYTE LINEAGE SPECIFIC ANTIGEN GP100) (MELANOMA-ASSOCIATED ME20 ANTIGEN) (ME20M/ME20S) (ME20-M/ME20-S) (95 KD MELANOCYTE-SPECIFIC SECRETED GLYCOPROTEIN) - HOMO SAPIENS (HUMAN), 661 aa.\|pcls:SWISSPROT-ID:P40967 MELANOCYTE PROTEIN PMEL 17 PRECURSOR (MELANOCYTE LINEAGE-SPECIFIC ANTIGEN GP100) (MELANOMA-ASSOCIATED ME20 ANTIGEN) (ME20M) (ME20-M / ME20-S) (95 KD MELANOCYTE-SPECIFIC SECRETED GLYCOPROTEIN) - HOMO SAPIENS (HUMAN), 661 aa.	0.00E+00	12
165	cg43286488	1841	CTGGCTGTCCTCCCCACACCTGGCT[C/A]CCATTGATGATGGTATTGTTGACCC	C	A	Gly	Gly	SILENT-CODING	glycoprotein	Human Gene SWISSNEW-ID:P40967 MELANOCYTE PROTEIN PMEL 17 PRECURSOR (MELANOCYTE LINEAGE SPECIFIC ANTIGEN GP100) (MELANOMA-ASSOCIATED ME20 ANTIGEN) (ME20M/ME20S) (ME20-M/ME20-S) (95 KD MELANOCYTE-SPECIFIC SECRETED GLYCOPROTEIN) - HOMO SAPIENS (HUMAN), 661 aa.\|pcls:SWISSPROT-ID:P40967 MELANOCYTE PROTEIN PMEL 17 PRECURSOR (MELANOCYTE LINEAGE-SPECIFIC ANTIGEN GP100) (MELANOMA-ASSOCIATED ME20 ANTIGEN) (ME20M) (ME20-M / ME20-S) (95 KD MELANOCYTE-SPECIFIC SECRETED GLYCOPROTEIN) - HOMO SAPIENS (HUMAN), 661 aa.	0.00E+00	12

166	cg43943531	1102	CTCCCTGGACG GGGCGTTTCTAC TC[G/A]CTGCTG GATCCCTCTTAT GCTAAGA	G	A	Ser	Ser	SILENT-CODING	glycoprotein	Human Gene SWISSPROT-ID:P46978 OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG (B5) (INTEGRAL MEMBRANE PROTEIN 1) - MUS MUSCULUS (MOUSE), 705 aa.	0.00E+00	11 (11q23.3)
167	cg43943531	1417	ACATGAAGAATC TGGACATAAGTC G[T/C]CCAGACAA GAAGAGCAAGAA GCAAC	T	C	Arg	Arg	SILENT-CODING	glycoprotein	Human Gene SWISSPROT-ID:P46978 OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG (B5) (INTEGRAL MEMBRANE PROTEIN 1) - MUS MUSCULUS (MOUSE), 705 aa.	0	11 (11q23.3)
168	cg43943531	847	CCTACTGTACTG TTTACTGCCTGG G[C/T]ACTATACT TTCTATGCAGAT CTCCT	C	T	Gly	Gly	SILENT-CODING	glycoprotein	Human Gene SWISSPROT-ID:P46978 OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG (B5) (INTEGRAL MEMBRANE PROTEIN 1) - MUS MUSCULUS (MOUSE), 705 aa.	0	11 (11q23.3)
169	cg43943531	916	TCCTTTCATCAG AGCACATGGCAG C[C/G]TTTGGGG TCTTTGGTCTCT GCCAGA	C	G	Ala	Ala	SILENT-CODING	glycoprotein	Human Gene SWISSPROT-ID:P46978 OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG (B5) (INTEGRAL MEMBRANE PROTEIN 1) - MUS MUSCULUS (MOUSE), 705 aa.	0	11 (11q23.3)
170	cg43065490	2042	AAGCAGAGCAGT ATCAACCCCTCA C[G/A]CGTTCAGT CAGCCTCCAGAA CTCCC	G	A	Thr	Thr	SILENT-CODING	glycoprotein	Human Gene SWISSPROT-ID:P16452 ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2 (P4.2) (PALLIDIN) - HOMO SAPIENS (HUMAN), 690 aa.	0	15 (15q15)
171	cg43065549	1597	AGGGTTATGATG GATGGCAGATTC T[C/G]GACCCAA GTGCTCCTAATG GAGGTG	C	G	Leu	Leu	SILENT-CODING	glycoprotein	Human Gene SWISSPROT-ID:P16452 ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2 (P4.2) (PALLIDIN) - HOMO SAPIENS (HUMAN), 690 aa.	0	15 (15q15)
172	cg43065549	1648	GAGTCCTGGGG TCCTGTGATCTG GT[A/G]CCGGTC AGAGCAGTCAAG GAGGGGA	A	G	Val	Val	SILENT-CODING	glycoprotein	Human Gene SWISSPROT-ID:P16452 ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2 (P4.2) (PALLIDIN) - HOMO SAPIENS (HUMAN), 690 aa.	0	15 (15q15)

173	cg43065549	1675	CGGTCAGAGCA GTCAAGGAGGG GAC[G/C]CTGGG GCTGACCCCAG CAGTGTCAG	G	C	Thr	Thr	SILENT-CODING	glycoprotein	Human Gene SWISSPROT-ID:P16452 ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2 (P4.2) (PALLIDIN) - HOMO SAPIENS (HUMAN), 690 aa.	0	15 (15q15)
174	cg43018621	507	CGGACAACCTG GAGCTGAAGAAG CT[G/A]GTATACC TCTACTTGATGA ATTACG	G	A	Leu	Leu	SILENT-CODING	glycoprotein	Human Gene SWISSNEW-ID:Q10567 BETA-ADAPTIN 1 (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN BETA SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 BETA LARGE CHAIN) (AP105A) - HOMO SAPIENS (HUMAN), 949 aa.\|pcls:SWISSPROT-ID:Q10567 BETA-ADAPTIN 1 (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN BETA SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 BETA LARGE CHAIN) (AP105A) - HOMO SAPIENS (HUMAN), 949 aa.	0	22 (22q12)
175	cg43924995	456	CAAAATGGCAGA TGAATTTCACAG T[A/T]CGCTATGA AACTACAAATAA AACTT	A	T	Val	Val	SILENT-CODING	glycoprotein	Human Gene SWISSPROT-ID:P13473 LYSOSOME-ASSOCIATED MEMBRANE GLYCOPROTEIN 2 PRECURSOR (LAMP-2) (CD107B ANTIGEN) - HOMO SAPIENS (HUMAN), 410 aa.	1.2E-222	X (Xq24)
176	cg43301245	1420	GCCCATCAAAGC CATGGGTGCGC AG[A/G]AATGGC GGTACTGACTTG ATGAAAG	A	G	Phe	Phe	SILENT-CODING	glycoprotein	Human Gene SWISSNEW-ID:P36222 CARTILAGE GLYCOPROTEIN-39 PRECURSOR (GP-39) (39 KD SYNOVIAL PROTEIN) (YKL-40) (CHITINASE-3 LIKE 1) - HOMO SAPIENS (HUMAN), 383 aa.\|pcls:SWISSPROT-ID:P36222 CARTILAGE GLYCOPROTEIN-39 PRECURSOR (GP-39) (39 KD SYNOVIAL PROTEIN) (YKL-40) - HOMO SAPIENS (HUMAN), 383 aa.	3E-210	1

177	cg43301245	757	GGTCCAGGGCC CATACCATGGCG CC[C/T]GCCAGC TGCCTGTCCTTC AGGTACT	C	T	Ala	Ala	SILENT-CODING	glycoprotein	Human Gene SWISSNEW-ID:P36222 CARTILAGE GLYCOPROTEIN-39 PRECURSOR (GP-39) (39 KD SYNOVIAL PROTEIN) (YKL-40) (CHITINASE-3 LIKE 1) - HOMO SAPIENS (HUMAN), 383 aa.\|pcls:SWISSPROT-ID:P36222 CARTILAGE GLYCOPROTEIN-39 PRECURSOR (GP-39) (39 KD SYNOVIAL PROTEIN) (YKL-40) - HOMO SAPIENS (HUMAN), 383 aa.	3E-210	1
178	cg43301245	769	ATACCATGGCGC CCGCCAGCTGC CT[G/A]TCCTTCA GGTACTGCACCT TGCTTT	G	A	Asp	Asp	SILENT-CODING	glycoprotein	Human Gene SWISSNEW-ID:P36222 CARTILAGE GLYCOPROTEIN-39 PRECURSOR (GP-39) (39 KD SYNOVIAL PROTEIN) (YKL-40) (CHITINASE-3 LIKE 1) - HOMO SAPIENS (HUMAN), 383 aa.\|pcls:SWISSPROT-ID:P36222 CARTILAGE GLYCOPROTEIN-39 PRECURSOR (GP-39) (39 KD SYNOVIAL PROTEIN) (YKL-40) - HOMO SAPIENS (HUMAN), 383 aa.	3E-210	1
179	cg43059879	580	TTACTTCCCTGC ATTCTGGTAATTT [A/T]GTCCAATTT CCATGTGTCGTG CAGG	A	T	Thr	Thr	SILENT-CODING	glycoprotein	Human Gene SWISSNEW-ID:P02749 BETA-2-GLYCOPROTEIN I PRECURSOR (APOLIPOPROTEIN H) (APO-H) (ACTIVATED PROTEIN C-BINDING PROTEIN) (APC INHIBITOR) - HOMO SAPIENS (HUMAN), 345 aa.\|pcls:SWISSPROT-ID:P02749 BETA-2-GLYCOPROTEIN I PRECURSOR (APOLIPOPROTEIN H) (APO-H) (ACTIVATED PROTEIN C-BINDING PROTEIN) (APC INHIBITOR) - HOMO SAPIENS (HUMAN), 345 aa.\|pcls:TREMBLNEW-ID:E308445 BETA-2-GLYCOPROTEIN I PRECURSOR - HOMO SAPIENS (HUMAN), 345 aa.	6.6E-199	17 (17q23)

180	cg43932434	1575	TGGGGTGGATC CGGGGAATCAC CAC[A/G]TGCCCT TCTATGAACCCA TACCTGC	A	G	His	His	SILENT-CODING	glycoprotein	Human Gene SWISSPROT-ID:P16070 CD44 ANTIGEN PRECURSOR (PHAGOCYTIC GLYCOPROTEIN I) (PGP-1) (HUTCH-I) (EXTRACELLULAR MATRIX RECEPTOR-III) (ECMR-III) (GP90 LYMPHOCYTE HOMING/ADHESION RECEPTOR) (HERMES ANTIGEN) (HYALURONATE RECEPTOR) (HEPARAN SULFATE PROTEOGLYCAN) (EPICAN) (CDW44) - HOMO SAPIENS (HUMAN), 742 aa.	1.8E-195	11 (11pter)
181	cg43988092	1994	TGAAGTTTCCAG TACTGAAATCCA G[C/T]TTCTGATT TTCTGCTCTTGC AAGGC	C	T	Lys	Lys	SILENT-CODING	glycoprotein	Human Gene SWISSPROT-ID:Q01685 TRAM PROTEIN (TRANSLOCATING CHAIN-ASSOCIATING MEMBRANE PROTEIN) - CANIS FAMILIARIS (DOG), 373 aa.	4E-192	8
182	cg43918166	2106	AACCATCTTTGC AGTGGTATCTAA T[C/A]AGGGAGTT GATTTCATAACG AGGTT	C	A	Leu	Leu	SILENT-CODING	glycoprotein	Human Gene SWISSPROT-ID:P55067 NEUROCAN CORE PROTEIN PRECURSOR (245 KD EARLY POSTNATAL CORE GLYCOPROTEIN) (CONTAINS: 150 KD ADULT CORE GLYCOPROTEIN) - RATTUS NORVEGICUS (RAT), 1257 aa.	4.5E-190	5
183	cg44022653	1149	TCTCAGCCTCGG AACAGTTGTGGG T[A/G]CCCAGTG CACACTCATCCA CGTCCT	A	G	Gly	Gly	SILENT-CODING	glycoprotein	Human Gene SWISSPROT-ID:Q08878 FIBULIN-1, ISOFORM C PRECURSOR (BASEMENT-MEMBRANE PROTEIN 90) (BM-90) - MUS MUSCULUS (MOUSE), 685 aa.	2.80E-188	3 (3p25)

184	cg43076975	1141	TGAATATGCTAA GGGAGTATCTTA G[T/C]GCTGACG CATTTAAAAGTG GTATTG	T	C	Ser	Ser	SILENT-CODING	glycoprotein	Human Gene Homologous to SWISSNEW-ID:P15144 AMINOPEPTIDASE N (EC 3.4.11.2) (MICROSOMAL AMINOPEPTIDASE) (GP150) (MYELOID PLASMA MEMBRANE GLYCOPROTEIN CD13) - HOMO SAPIENS (HUMAN), 966 aa.\|pcls:SWISSPROT-ID:P15144 AMINOPEPTIDASE N (EC 3.4.11.2) (MICROSOMAL AMINOPEPTIDASE) (GP150) (MYELOID PLASMA MEMBRANE GLYCOPROTEIN CD13) - HOMO SAPIENS (HUMAN), 966 aa.	3.40E-120		5
185	cg43051796	1072	AGGTGAACATCG CAAATCGCTTCC C[A/G]CAGCCCT CGTTGCCGCAG CACCCAC	A	G	Cys	Cys	SILENT-CODING	glycoprotein	Human Gene Homologous to SWISSNEW-ID:P48230 TETRASPAN MEMBRANE PROTEIN IL-TMP - HOMO SAPIENS (HUMAN), 202 aa.\|pcls:SWISSPROT-ID:P48230 TETRASPAN MEMBRANE PROTEIN IL-TMP - HOMO SAPIENS (HUMAN), 202 aa.	4.00E-114		3
186	cg43287997	330	TGGGCCTCTGCC TCTTATCAGTTG G[C/T]GTTTGGG GGCAAGATGGTA ATGAAG	C	T	Gly	Gly	SILENT-CODING	glycoprotein	Human Gene Homologous to SWISSNEW-ID:P07766 T-CELL SURFACE GLYCOPROTEIN CD3 EPSILON CHAIN PRECURSOR (T-CELL SURFACE ANTIGEN T3/LEU-4 EPSILON CHAIN) - HOMO SAPIENS (HUMAN), 207 aa.\|pcls:SWISSPROT-ID:P07766 T-CELL SURFACE GLYCOPROTEIN CD3 EPSILON CHAIN PRECURSOR (T-CELL SURFACE ANTIGEN T3/LEU-4 EPSILON CHAIN) - HOMO SAPIENS (HUMAN), 207 aa.	1.30E-113	11 (11q23)	

187	cg43959140	705	TTTCCCTGCGGC TATCACAAAATG G[A/G]GTATACCC ATAAGGAGCTCC ATCCA	A	G	Thr	Thr	SILENT-CODING	glycoprotein	Human Gene Homologous to SWISSPROT-ID:Q09332 UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-) (DUGT) - DROSOPHILA MELANOGASTER (FRUIT FLY), 1548 aa.	1.30E-108	
188	cg36834323	312	ACCCTGCAGATG CTAAGAATGCTG C[G/C]AAAGATAT GAATGGAAAGTC TTTGC	G	C	Ala	Ala	SILENT-CODING	glycoprotein	Human Gene Similar to SWISSPROT-ID:P38159 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN G (HNRNP G) (GLYCOPROTEIN P43) - HOMO SAPIENS (HUMAN), 437 aa.	6.40E-91	
189	cg44019290	1506	CCGTGGCCTGG AGGAGGGAGAG GGA[G/C]AGCAG GAGCAGCAGCA GCCACGAGG	G	C	Leu	Leu	SILENT-CODING	glycoprotein	Human Gene Similar to SWISSPROT-ID:P04216 THY-1 MEMBRANE GLYCOPROTEIN PRECURSOR (THY-1 ANTIGEN) (CDW90) (CD90 ANTIGEN) - HOMO SAPIENS (HUMAN), 161 aa.	2.50E-80	11
190	cg44924334	506	CCACCTGCCAGT CTATTGCCTTCC C[C/T]AGCAAGAC CTCTGCCAGTAT AGGCA	C	T	Pro	Pro	SILENT-CODING	glycoprotein	Human Gene Similar to SWISSPROT-ID:Q13491 NEURONAL MEMBRANE GLYCOPROTEIN M6-B - HOMO SAPIENS (HUMAN), 283 aa (fragment).	5.60E-76	
191	cg44924334	674	ACCTGTTTATTG CTGCATTTGTGG G[G/T]GCTGCAG CTACACTGGTTT CCCTGC	G	T	Gly	Gly	SILENT-CODING	glycoprotein	Human Gene Similar to SWISSPROT-ID:Q13491 NEURONAL MEMBRANE GLYCOPROTEIN M6-B - HOMO SAPIENS (HUMAN), 283 aa (fragment).	5.60E-76	
192	cg41568631	1548	CTGTGGAGTCCA TCAAGAATGGCC T[G/C]GTCTACAT GAAGTACGACAC GCCTT	G	C	Leu	Leu	SILENT-CODING	glycoprotein	Human Gene Similar to SWISSPROT-ID:P16452 ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2 (P4.2) (PALLIDIN) - HOMO SAPIENS (HUMAN), 690 aa.	9.90E-70	14 (14q11.2)
193	cg43918233	1133	CTGCCTCCAGTG AGAACCGTGAAG G[A/G]ACACTTTC GGATTCCACGG GTAGCG	A	G	Gly	Gly	SILENT-CODING	glycoprotein	Human Gene Similar to SPTREMBL-ID:Q63575 TRANS GOLGI NETWORK (TGN) SPECIFIC INTEGRAL MEMBRANE PROTEIN TGN38 PRECURSOR - RATTUS NORVEGICUS (RAT), 380 aa.	7.60E-67	2

194	cg43965366	2066	TCACGTCGAACG TCTCCTTCTTGA A[T/C]TCTGCCTT CGGGACCCCGG TGTAGA	T	C	Glu	Glu	SILENT-CODING	glycoprotein	Human Gene Similar to SWISSPROT-ID:P49222 ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2 (P4.2) (PALLIDIN) - MUS MUSCULUS (MOUSE), 690 aa.	8.90E-61	6 (6p25)
195	cg43982558	1326	AGGCTGCAGTG CGCTTCGTGGGT TT[C/T]CCAGATA AAAAGCATAAGC TGTATG	C	T	Phe	Phe	SILENT-CODING	glycoprotein	Human Gene Similar to SWISSPROT-ID:P55067 NEUROCAN CORE PROTEIN PRECURSOR (245 KD EARLY POSTNATAL CORE GLYCOPROTEIN) (CONTAINS: 150 KD ADULT CORE GLYCOPROTEIN) - RATTUS NORVEGICUS (RAT), 1257 aa.	2.10E-53	5 (5q13)
196	cg41603916	259	TCACCTGGCGCT ACCAGCCCGAA GG[G/A]GGCAGA GATGCCATTTCG ATCTTCC	G	A	Gly	Gly	SILENT-CODING	glycoprotein	Human Gene Similar to SPTREMBL-ID:Q91406 IP1=CNS MYELIN P0-LIKE GLYCOPROTEIN - UNKNOWN, 202 aa.	3.00E-52	1 (1q22)
197	cg43250682	1520	TTCTGACTCCAA AAATCAACCAGA C[G/C]TTTAGCG GGATCATGACTA TGTTGA	G	C	Thr	Thr	SILENT-CODING	Guanylyl	Human Gene SWISSPROT-ID:P19687 GUANYLATE CYCLASE SOLUBLE, ALPHA-1 CHAIN (EC 4.6.1.2) (73 KD CHAIN) - BOS TAURUS (BOVINE), 691 aa.	0.00E+00	4
198	cg43250682	2120	AGACCATTGGCG ATGCCTATTGTG T[G/A]GCTGGGG GATTACACAAAG AGAGTG	G	A	Val	Val	SILENT-CODING	Guanylyl	Human Gene SWISSPROT-ID:P19687 GUANYLATE CYCLASE SOLUBLE, ALPHA-1 CHAIN (EC 4.6.1.2) (73 KD CHAIN) - BOS TAURUS (BOVINE), 691 aa.	0.00E+00	4
199	cg43956596	1584	GCATTGTCTTCA CCAAGCAGCCG GA[A/G]CCGGTG ATTCCAGTGAAG GATGCCA	A	G	Glu	Glu	SILENT-CODING	helicase	Human Gene SWISSNEW-ID:Q92620 PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE KIAA0224 (HA4657) - HOMO SAPIENS (HUMAN), 1227 aa.\|pcls:SWISSPROT-ID:Q92620 PUTATIVE ATP-DEPENDENT RNA HELICASE KIAA0224 (HA4657) - HOMO SAPIENS (HUMAN), 1227 aa.	0.00E+00	16

200	cg43956596	1587	TTGTCTTCACCA AGCAGCCGGAA CC[G/A]GTGATTC CAGTGAAGGATG CCACTT	G	A	Pro	Pro	SILENT-CODING	helicase	Human Gene SWISSNEW-ID:Q92620 PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE KIAA0224 (HA4657) - HOMO SAPIENS (HUMAN), 1227 aa.\|pcls:SWISSPROT-ID:Q92620 PUTATIVE ATP-DEPENDENT RNA HELICASE KIAA0224 (HA4657) - HOMO SAPIENS (HUMAN), 1227 aa.	0.00E+00	16
201	cg43956596	718	CAGTCGGCAGA GAGAGCGGGAG CGG[C/A]GGGAA CATGGTGTCTAT GCCTCGTC	C	A	Arg	Arg	SILENT-CODING	helicase	Human Gene SWISSNEW-ID:Q92620 PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE KIAA0224 (HA4657) - HOMO SAPIENS (HUMAN), 1227 aa.\|pcls:SWISSPROT-ID:Q92620 PUTATIVE ATP-DEPENDENT RNA HELICASE KIAA0224 (HA4657) - HOMO SAPIENS (HUMAN), 1227 aa.	0	16
202	cg43931167	2037	ATGACTTTGGCT GGGGAGTAGTG GT[A/G]AATTTCT CAAAAAAGTCAA ATGTTA	A	G	Val	Val	SILENT-CODING	helicase	Human Gene SWISSPROT-ID:O14232 PUTATIVE HELICASE C6F12.16 IN CHROMOSOME I - SCHIZOSACCHAROMYCES POMBE (FISSION YEAST), 1117 aa.	3.3E-307	5
203	cg43958815	720	GCTTCTTCCGCT TCTTGTGAGGGC G[T/C]ACCAGGC CACGGAGAGCA GGAGGAA	T	C	Val	Val	SILENT-CODING	helicase	Human Gene Similar to SWISSPROT-ID:Q06218 PROBABLE ATP-DEPENDENT RNA HELICASE DBP9 - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 594 aa.	3.9E-100	
204	cg43263560	544	ACAAAACCCTTG CTTTAATTAAAGA [C/T]GGCCGTGTT ATTGGTGGTATC TGTT	C	T	Asp	Asp	SILENT-CODING	histone	Human Gene Similar to TREMBLNEW-ID:G2707336 HISTONE ACETYLTRANSFERASE - ARABIDOPSIS THALIANA (MOUSE-EAR CRESS), 418 aa.	3E-61	3
205	cg43988803	1992	GACATGCTCAGC AGACATCTGCAG T[T/C]AACGGGC GTCCCCTGCCCC ACACGG	T	C	Val	Val	SILENT-CODING	homeobox	Human Gene SPTREMBL-ID:Q12776 PAX-3-FKHR GENE FUSION - HOMO SAPIENS (HUMAN), 689 aa (fragment).	1.2E-242	13 (13q14.1)

206	cg43332152	981	ACCTGGGCGCC AAGCGGCGGGG ACC[G/C]CGCAC CACCATCAAAGC CAAGCAGC	G	C	Pro	Pro	SILENT-CODING	homeobox	Human Gene SWISSPROT-ID:P36199 HOMEOBOX PROTEIN LIM-1 (HOMEOBOX PROTEIN LMX-2) - MUS MUSCULUS (MOUSE), RATTUS NORVEGICUS (RAT), AND MESOCRICETUS, 406 aa.	3.4E-227	17
207	cg41637704	1201	AGGAGCTGCTG GGGCCGCCAGC GCC[G/C]CGAGA CAAGGGCAGCG GACCGCCTG	G	C	Pro	Pro	SILENT-CODING	homeobox	Human Gene SWISSPROT-ID:P50219 HOMEOBOX PROTEIN HB9 - HOMO SAPIENS (HUMAN), 401 aa.	1.2E-224	7
208	cg43143467	581	CTTTCAACCATC TCATTCCCGGGG G[G/A]TTCCCTCC CACTGCCATGCC GACCT	G	A	Gly	Gly	SILENT-CODING	homeobox	Human Gene SPTREMBL-ID:Q12777 PAX-3 - HOMO SAPIENS (HUMAN), 332 aa (fragment).	2.1E-179	2 (2q35)
209	cg43971192	625	TGTTGAAAAGAC CACTCTGTGTAT T[C/G]GTACTTGG TCCAGATTTACA AGTGT	C	G	Thr	Thr	SILENT-CODING	homeobox	Human Gene Homologous to SWISSPROT-ID:Q15583 5'-TG-3' INTERACTING FACTOR (HOMEOBOX PROTEIN TGIF) - HOMO SAPIENS (HUMAN), 272 aa.	1.9E-144	18
210	cg40291306	693	AGATCAAGATCT GGTTCCAGAACC G[A/C]AGGATGA AGTGGAAGAAAG ATTCCA	A	C	Arg	Arg	SILENT-CODING	homeobox	Human Gene Homologous to SWISSPROT-ID:Q00444 HOMEOBOX PROTEIN HOX-C5 (HOX-3D) (CP11) - HOMO SAPIENS (HUMAN), 222 aa.	8.3E-121	12
211	cg40291306	694	GATCAAGATCTG GTTCCAGAACCG A[A/C]GGATGAA GTGGAAGAAAGA TTCCAA	A	C	Arg	Arg	SILENT-CODING	homeobox	Human Gene Homologous to SWISSPROT-ID:Q00444 HOMEOBOX PROTEIN HOX-C5 (HOX-3D) (CP11) - HOMO SAPIENS (HUMAN), 222 aa.	8.3E-121	12

212	cg43923497	1741	ACTTCACCTTCT CTGTGGCCAGG CA[C/T]TTGATCT TTTCCTCCACCA AGAAGC	C	T	Lys	Lys	SILENT-CODING	hydrolase	Human Gene SWISSPROT-ID:P45974 UBIQUITIN CARBOXYL-TERMINAL HYDROLASE T (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE T) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE T) (DEUBIQUITINATING ENZYME T) (ISOPEPTIDASE T) - HOMO SAPIENS (HUMAN), 858 aa.	0	12
213	cg43922794	2430	TTAAATGCCACC GAACCTATCGGC T[C/G]TTTGCAGT GGTCTACCATCA CGGCA	C	G	Leu	Leu	SILENT-CODING	hydrolase	Human Gene SWISSPROT-ID:Q14694 PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING ENZYME) (KIAA0190) - HOMO SAPIENS (HUMAN), 798 aa.	0.00E+00	14
214	cg43285385	616	TTAAGACATTGA AAAACTTCTTTAA [C/T]TTTTCATTC ATTGTAAAATTCT TCA	C	T	Lys	Lys	SILENT-CODING	hydrolase	Human Gene TREMBLNEW-ID:G2951931 HUMAN GAMMA-GLUTAMYL HYDROLASE (EC 3.4.22.12) - HOMO SAPIENS (HUMAN), 318 aa.	4.80E-173	8
215	cg43925670	1390	TTTTTCTAAGTC GAAAGCAGAAAA G[T/C]TGGAGCTT ATCTCCTTCTTC ACAGG	T	C	Gln	Gln	SILENT-CODING	interferon	Human Gene SWISSPROT-ID:Q16666 GAMMA-INTERFERON-INDUCIBLE PROTEIN IFI-16 (INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR) - HOMO SAPIENS (HUMAN), 729 aa.\|pcls:SPTREMBL-ID:Q16666 IFI16=INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR - HOMO SAPIENS (HUMAN), 729 aa (fragment).	0.00E+00	1

216	cg43925670	1720	ATATGATGATGATTTTCTTTCCATT[A/G]AATTTCTCCTTCAAGCTGGTGTTTA	A	G	Phe	Phe	SILENT-CODING	interferon	Human Gene SWISSPROT-ID:Q16666 GAMMA-INTERFERON-INDUCIBLE PROTEIN IFI-16 (INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR) - HOMO SAPIENS (HUMAN), 729 aa.\|pcls:SPTREMBL-ID:Q16666 IFI16=INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR - HOMO SAPIENS (HUMAN), 729 aa (fragment).	0.00E+00	1
217	cg43082514	921	CCAGCGATGAAGAGAGTGCCGAGGG[G/A]CGGCCACACTGGCGGAAGAGGAATA	G	A	Gly	Gly	SILENT-CODING	interferon	Human Gene SWISSPROT-ID:P14316 INTERFERON REGULATORY FACTOR 2 (IRF-2) - HOMO SAPIENS (HUMAN), 349 aa.	5.50E-188	4 (4q35.1)
218	cg43922672	1212	CTGCTGAAACATCTGCCTTGGACAC[A/G]GGGTTCTCGCTCAACCTTTCAGAGC	A	G	Thr	Thr	SILENT-CODING	interleukin	Human Gene TREMBLNEW-ID:G2114410 INTERLEUKIN-16 - HOMO SAPIENS (HUMAN), 631 aa.	0	15
219	cg42887911	402	CCCTGCCCACCCTGGCCATGAGTGC[A/G]GGGGCACTGGGAGCTCTACAGCTCC	A	G	Ala	Ala	SILENT-CODING	interleukin	Human Gene Homologous to SWISSPROT-ID:P20809 INTERLEUKIN-11 PRECURSOR (IL-11) (ADIPOGENESIS INHIBITORY FACTOR) (AGIF) - HOMO SAPIENS (HUMAN), 199 aa.	2.5E-103	19
220	cg43929155	434	TCCTATGCAAGGCAGTCCATGTCAT[C/T]TACACAGTCAACCTCTACAGCAGTG	C	T	Ile	Ile	SILENT-CODING	interleukinrecept	Human Gene Similar to SWISSPROT-ID:P21109 HIGH AFFINITY INTERLEUKIN-8 RECEPTOR A (IL-8R A) (CXCR-1) - ORYCTOLAGUS CUNICULUS (RABBIT), 355 aa.	4.2E-55	2
221	cg43951261	2559	AACAAGCATTGATGATGACTATTGT[A/G]AATTTGGCTCAGAACTTTGTGGGAA	A	G	Val	Val	SILENT-CODING	isomerase	Human Gene SWISSPROT-ID:Q02880 DNA TOPOISOMERASE II, BETA ISOZYME (EC 5.99.1.3) - HOMO SAPIENS (HUMAN), 1626 aa.	0	3 (3p)

222	cg43993971	1428	AGGCAATGATGA ACAGGGAGGAC TC[G/C]GGGTTC AGCTGGGCCAG GGTTTTGG	G	C	Pro	Pro	SILENT-CODING	isomerase	Human Gene SWISSPROT-ID:P06744 GLUCOSE-6-PHOSPHATE ISOMERASE (GPI) (EC 5.3.1.9) (PHOSPHOGLUCOSE ISOMERASE) (PGI) (PHOSPHOHEXOSE ISOMERASE) (PHI) (NEUROLEUKIN) (NLK) - HOMO SAPIENS (HUMAN), 558 aa.	3.60E-305	19 (19q13.1)
223	cg43930054	738	TCTGGGTTGTGG GTGTGCTGGCTA T[C/T]ACTGTCCC CTGTACCATCAG GAGGA	C	T	Val	Val	SILENT-CODING	isomerase	Human Gene SWISSPROT-ID:P34949 MANNOSE-6-PHOSPHATE ISOMERASE (EC 5.3.1.8) (PHOSPHOMANNOSE ISOMERASE) (PMI) (PHOSPHOHEXOMUTASE) - HOMO SAPIENS (HUMAN), 422 aa.	2.00E-222	15 (15q22)
224	cg43961450	1141	ACTCTGCCTTAG TCTTCTTTGCAA A[C/T]ACATCTGC AAACTTCTTCTTC ATTT	C	T	Val	Val	SILENT-CODING	isomerase	Human Gene Homologous to SWISSPROT-ID:P70473 2-ARYLPROPIONYL-COA EPIMERASE (EC 5.-.-.-) - RATTUS NORVEGICUS (RAT), 361 aa.	1.80E-117	5
225	cg43961450	1237	CAAGTCCAAGTC CTTTAAGCAGCA G[T/C]GCGTAGA ACTGGGGTTCTA TTGCTC	T	C	Ala	Ala	SILENT-CODING	isomerase	Human Gene Homologous to SWISSPROT-ID:P70473 2-ARYLPROPIONYL-COA EPIMERASE (EC 5.-.-.-) - RATTUS NORVEGICUS (RAT), 361 aa.	1.80E-117	5

226	cg43924460	609	TCATAAAGAGTG TTACACCGTGCG C[A/T]CCAAAGTA CCACAAAGCCTG CTCCA	A	T	Ala	Ala	SILENT-CODING	isomerase	Human Gene Similar to SWISSNEW-ID:Q27450 PEPTIDYLPROLYL ISOMERASE CYP-1 (EC 5.2.1.8) (PEPTIDYLPROLYL CIS-TRANS ISOMERASE) (CYCLOPHILIN) (PPIASE) - BRUGIA MALAYI, 843 aa.\|pcls:SWISSPROT-ID:Q27450 PEPTIDYLPROLYL ISOMERASE CYP-1 (EC 5.2.1.8) (PEPTIDYLPROLYL CIS-TRANS ISOMERASE) (CYCLOPHILIN) (PPIASE) - BRUGIA MALAYI, 843 aa.\|pcls:SPTREMBL-ID:Q27450 PEPTIDYLPROLYL ISOMERASE (EC 5.2.1.8) (PEPTIDYLPROLYL CIS-TRANS ISOMERASE) (CYCLOPHILIN) (PPIASE) - BRUGIA MALAYI, 843 aa.	4.20E-71	8 (8p22)
227	cg43145505	253	ACTTGATGCCCC CAAGAATCCTAG T[A/G]GAATGTTT ACTACCAAATGG AATGA	A	G	Val	Val	SILENT-CODING	kinase	Human Gene SWISSNEW-ID:P42336 PHOSPHATIDYLINOSITOL 3-KINASE CATALYTIC SUBUNIT, ALPHA ISOFORM (EC 2.7.1.137) (PI3-KINASE P110 SUBUNIT ALPHA) (PTDINS-3-KINASE P110) (PI3K) - HOMO SAPIENS (HUMAN), 1068 aa.\|pcls:SWISSPROT-ID:P42336 PHOSPHATIDYLINOSITOL 3-KINASE CATALYTIC SUBUNIT, ALPHA ISOFORM (EC 2.7.1.137) (PI3-KINASE P110 SUBUNIT ALPHA) (PTDINS-3-KINASE P110) (PI3K) - HOMO SAPIENS (HUMAN), 1068 aa.	0.00E+00	3

228	cg43145505	358	TATTTAAAGAAG CAAGAAAATACC C[C/T]CTCCATCA ACTTCTTCAAGA TGAAT	C	T	Pro	Pro	SILENT-CODING	kinase	Human Gene SWISSNEW-ID:P42336 PHOSPHATIDYLINOSITOL 3-KINASE CATALYTIC SUBUNIT, ALPHA ISOFORM (EC 2.7.1.137) (PI3-KINASE P110 SUBUNIT ALPHA) (PTDINS-3-KINASE P110) (PI3K) - HOMO SAPIENS (HUMAN), 1068 aa.\|pcls:SWISSPROT-ID:P42336 PHOSPHATIDYLINOSITOL 3-KINASE CATALYTIC SUBUNIT, ALPHA ISOFORM (EC 2.7.1.137) (PI3-KINASE P110 SUBUNIT ALPHA) (PTDINS-3-KINASE P110) (PI3K) - HOMO SAPIENS (HUMAN), 1068 aa.	0.00E+00	3
229	cg43918241	943	TGTCTAAAGAGT GTAAAGACCTAA T[C/T]ACACGGAT GCTACAGAGAGA TCCCA	C	T	Ile	Ile	SILENT-CODING	kinase	Human Gene SPTREMBL-ID:Q63553 SNF1-RELATED KINASE - RATTUS NORVEGICUS (RAT), 746 aa.	0.00E+00	3
230	cg43252989	2330	ATTTTGAGGTTT GGTTTTATGATG G[G/T]GTGAAACT ACACAAAATAGA AGATT	G	T	Gly	Gly	SILENT-CODING	kinase	Human Gene SPTREMBL-ID:O00444 SERINE/THREONINE PROTEIN KINASE - HOMO SAPIENS (HUMAN), 970 aa.	0.00E+00	4
231	cg43916734	18295	GCAGGCTATTGT TTATCCCTTCAC G[C/A]GAAGCAG CGAAAGCTATTC CTTCAA	C	A	Arg	Arg	SILENT-CODING	kinase	Human Gene SPTREMBL-ID:P78527 DNA-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT - HOMO SAPIENS (HUMAN), 4127 aa.	0.00E+00	8
232	cg43257400	2027	TTGCCTGTACAC AGAGTTCTGCCC G[G/C]TCCCTTGT AGGATCCAGTCT AGAAG	G	C	Arg	Arg	SILENT-CODING	kinase	Human Gene SPTREMBL-ID:Q60680 CONSERVED HELIX-LOOP-HELIX UBIQUITOUS KINASE - MUS MUSCULUS (MOUSE), 745 aa.	0.00E+00	10
233	cg43329663	2266	CTCGAGAGGCC AACCCAGAGAAA TT[T/C]AACAGCC GCTTTCGGAATA AGATGT	T	C	Phe	Phe	SILENT-CODING	kinase	Human Gene SPTREMBL-ID:O00542 DIACYLGLYCEROL KINASE ZETA - HOMO SAPIENS (HUMAN), 1117 aa.	0.00E+00	11

234	cg43151490	322	ATCTGACGGTGA GCGTGGACCAG GT[A/G]CGCGTG GGCCAGACCAG CACAAAGC	A	G	Val	Val	SILENT-CODING	kinase	Human Gene SWISSPROT-ID:P24723 PROTEIN KINASE C, ETA TYPE (EC 2.7.1.-) (NPKC-ETA) (PKC-L) - HOMO SAPIENS (HUMAN), 682 aa.	0.00E+00	14
235	cg44929725	2320	TGGATCTCTTCA TGCACCGGAAAA G[C/T]GATGTCCT TACCACACCATG GAAAT	C	T	Ser	Ser	SILENT-CODING	kinase	Human Gene SWISSPROT-ID:P23458 TYROSINE-PROTEIN KINASE JAK1 (EC 2.7.1.112) (JANUS KINASE 1) (JAK-1) - HOMO SAPIENS (HUMAN), 1142 aa.	0.00E+00	1 (1p31.3)
236	cg44929725	2347	ATGTCCTTACCA CACCATGGAAAT T[T/C]AAAGTTGC CAAACAGCTGGC CAGTG	T	C	Phe	Phe	SILENT-CODING	kinase	Human Gene SWISSPROT-ID:P23458 TYROSINE-PROTEIN KINASE JAK1 (EC 2.7.1.112) (JANUS KINASE 1) (JAK-1) - HOMO SAPIENS (HUMAN), 1142 aa.	0.00E+00	1 (1p31.3)
237	cg44929725	2449	AAAACCTCCTCC TGGCCCGTGAG GG[C/A]ATCGAC AGTGAGTGTGGC CCATTCA	C	A	Gly	Gly	SILENT-CODING	kinase	Human Gene SWISSPROT-ID:P23458 TYROSINE-PROTEIN KINASE JAK1 (EC 2.7.1.112) (JANUS KINASE 1) (JAK-1) - HOMO SAPIENS (HUMAN), 1142 aa.	0.00E+00	1 (1p31.3)
238	cg44929725	2884	CTGAAGTGGACC CCACACATTTTG A[A/G]AAGCGCTT CCTAAAGAGGAT CCGTG	A	G	Glu	Glu	SILENT-CODING	kinase	Human Gene SWISSPROT-ID:P23458 TYROSINE-PROTEIN KINASE JAK1 (EC 2.7.1.112) (JANUS KINASE 1) (JAK-1) - HOMO SAPIENS (HUMAN), 1142 aa.	0.00E+00	1 (1p31.3)
239	cg44929725	3649	CTAACTGTCCAG ATGAGGTTTATC A[A/G]CTTATGAG GAAATGCTGGGA ATTCC	A	G	Gln	Gln	SILENT-CODING	kinase	Human Gene SWISSPROT-ID:P23458 TYROSINE-PROTEIN KINASE JAK1 (EC 2.7.1.112) (JANUS KINASE 1) (JAK-1) - HOMO SAPIENS (HUMAN), 1142 aa.	0.00E+00	1 (1p31.3)
240	cg44929725	3658	CAGATGAGGTTT ATCAACTTATGA G[G/A]AAATGCTG GGAATTCCAACC ATCCA	G	A	Arg	Arg	SILENT-CODING	kinase	Human Gene SWISSPROT-ID:P23458 TYROSINE-PROTEIN KINASE JAK1 (EC 2.7.1.112) (JANUS KINASE 1) (JAK-1) - HOMO SAPIENS (HUMAN), 1142 aa.	0.00E+00	1 (1p31.3)

241	cg44918305	1129	TGAGTACTCGCACAGAAGCATTAGA[A/G]GCCTTACAGAGTGAAAAATCACGAA	A	G	Glu	Glu	SILENT-CODING	kinase	Human Gene SPTREMBL-ID:Q03962 RET PROTO-ONCOGENE TYROSINE KINASE 2 (EC 2.7.1.112) - HOMO SAPIENS (HUMAN), 899 aa.	0.00E+00	10 (10q11.2)
242	cg43940596	1642	TCTTCACGCACAAGGGGTGGTTCAT[A/C]GAGACTTGAAACCTAGCAACATTCT	A	C	Arg	Arg	SILENT-CODING	kinase	Human Gene SWISSPROT-ID:P51812 RIBOSOMAL PROTEIN S6 KINASE II ALPHA 2 (EC 2.7.1.-) (S6KII-ALPHA) (P90-RSK 2) (INSULIN-STIMULATED PROTEIN KINASE 1) (ISPK-1) - HOMO SAPIENS (HUMAN), 740 aa.	0.00E+00	X
243	cg43931272	2078	GTTCTTTCCCAACCACAAAACACTC[C/T]GGTGGTAAATACCAATAAGTACCAG	C	T	Pro	Pro	SILENT-CODING	kinase	Human Gene TREMBLNEW-ID:G2853031 TOUSLED-LIKE KINASE - MUS MUSCULUS (MOUSE), 717 aa.	0.00E+00	
244	cg43930294	1630	TAGCTGGTTGATGAGAAGCATGCCC[T/C]TGTATATCACTTGTTAACTTGGGAG	T	C	Gln	Gln	SILENT-CODING	kinase	Human Gene SPTREMBL-ID:O00311 CDC7-RELATED KINASE - HOMO SAPIENS (HUMAN), 574 aa.	2.90E-308	1
245	cg43952792	1125	TCCGCGAGAGTGAAACCACCAAAGG[T/G]GCCTATTCACTTTCTATCCGTGATT	T	G	Gly	Gly	SILENT-CODING	kinase	Human Gene SWISSPROT-ID:P06241 PROTO-ONCOGENE TYROSINE-PROTEIN KINASE FYN (EC 2.7.1.112) (P59-FYN) (SYN) (SLK) - HOMO SAPIENS (HUMAN), 536 aa.	4.30E-300	6 (6q21)
246	cg43922705	3970	TCTGCTGGTCCAGGGTATGCAGGAA[G/A]GCTGAGTTGGGGTCCAGGGTGCGCT	G	A	Ala	Ala	SILENT-CODING	kinase	Human Gene SWISSPROT-ID:P27987 1D-MYO-INOSITOL-TRISPHOSPHATE 3 KINASE B (EC 2.7.1.127) (INOSITOL 1,4,5-TRISPHOSPHATE 3-KINASE) (IP3K) (IP3 3-KINASE) - HOMO SAPIENS (HUMAN), 505 aa (fragment).	3.80E-279	1 (1q41)
247	cg43241753	1745	CCTGTGTGTGGCTTGTTTCATTCAT[A/G]TGTTTGGAAACCAGGTTACCAACAT	A	G	His	His	SILENT-CODING	kinase	Human Gene SPTREMBL-ID:Q16675 PROTEIN-TYROSINE KINASE PRECURSOR - HOMO SAPIENS (HUMAN), 477 aa.	4.20E-268	9

248	cg43965549	625	GCGCCTTTGGAA AGGTATACTTGG C[A/T]CAAGATAT AAAGACGAAGAA AAGAA	A	T	Ala	Ala	SILENT-CODING	kinase	Human Gene SWISSPROT-ID:P41279 COT PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1.-) (C-COT) (CANCER OSAKA THYROID ONCOGENE) - HOMO SAPIENS (HUMAN), 467 aa.	2.30E-253	10 (10p11.2)	
249	cg43965549	703	AATTTAAGCCAT CTGATGTGGAAA T[C/T]CAGGCTTG CTTCCGGCACGA GAACA	C	T	Ile	Ile	SILENT-CODING	kinase	Human Gene SWISSPROT-ID:P41279 COT PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1.-) (C-COT) (CANCER OSAKA THYROID ONCOGENE) - HOMO SAPIENS (HUMAN), 467 aa.	2.30E-253	10 (10p11.2)	
250	cg43926820	1479	CATACAGGATGC AACCCAAGGACC A[G/T]ATGTCACT TTTATTGTTATAA GGCA	G	T	Ile	Ile	SILENT-CODING	kinase	Human Gene SWISSPROT-ID:P51956 SERINE/THREONINE-PROTEIN KINASE NEK3 (EC 2.7.1.-) (NIMA-RELATED PROTEIN KINASE 3) (HSPK 36) - HOMO SAPIENS (HUMAN), 459 aa (fragment).	1.40E-251	13	
251	cg43069976	469	TGGCTAGTGTAA TTACAAAGGGAA C[C/G]AAGGAAA GGCAATACTTAG ATGAAG	C	G	Thr	Thr	SILENT-CODING	kinase	Human Gene SWISSNEW-ID:P51955 SERINE/THREONINE-PROTEIN KINASE NEK2 (EC 2.7.1.-) (NIMA-RELATED PROTEIN KINASE 2) (NIMA-LIKE PROTEIN KINASE 1) (HSPK 21) - HOMO SAPIENS (HUMAN), 445 aa.\pds:SWISSPROT-ID:P51955 SERINE/THREONINE-PROTEIN KINASE NEK2 (EC 2.7.1.-) (NIMA-RELATED PROTEIN KINASE 2) (NIMA-LIKE PROTEIN KINASE 1) (HSPK 21) - HOMO SAPIENS (HUMAN), 445 aa.	3.00E-235	1	

252	cg43069976	589	GTCATACCGTAT TGCATCGGGATC T[G/T]AAACCAGC CAATGTTTTCCT GGATG	G	T	Leu	Leu	SILENT-CODING	kinase	Human Gene SWISSNEW-ID:P51955 SERINE/THREONINE-PROTEIN KINASE NEK2 (EC 2.7.1.-) (NIMA-RELATED PROTEIN KINASE 2) (NIMA-LIKE PROTEIN KINASE 1) (HSPK 21) - HOMO SAPIENS (HUMAN), 445 aa.\|pcls:SWISSPROT-ID:P51955 SERINE/THREONINE-PROTEIN KINASE NEK2 (EC 2.7.1.-) (NIMA-RELATED PROTEIN KINASE 2) (NIMA-LIKE PROTEIN KINASE 1) (HSPK 21) - HOMO SAPIENS (HUMAN), 445 aa.	3.00E-235	1
253	cg43069976	667	TTGGGCTAGCTA GAATATTAAACC A[T/C]GACACGA GTTTTGCAAAAA CATTTG	T	C	His	His	SILENT-CODING	kinase	Human Gene SWISSNEW-ID:P51955 SERINE/THREONINE-PROTEIN KINASE NEK2 (EC 2.7.1.-) (NIMA-RELATED PROTEIN KINASE 2) (NIMA-LIKE PROTEIN KINASE 1) (HSPK 21) - HOMO SAPIENS (HUMAN), 445 aa.\|pcls:SWISSPROT-ID:P51955 SERINE/THREONINE-PROTEIN KINASE NEK2 (EC 2.7.1.-) (NIMA-RELATED PROTEIN KINASE 2) (NIMA-LIKE PROTEIN KINASE 1) (HSPK 21) - HOMO SAPIENS (HUMAN), 445 aa.	3.00E-235	1
254	cg43967889	1159	AATTACGGGACC CAAATGTCAAAC T[A/T]CCAAATGG GCGAGACACAC CTGCAC	A	T	Leu	Leu	SILENT-CODING	kinase	Human Gene SWISSPROT-ID:P49841 GLYCOGEN SYNTHASE KINASE-3 BETA (EC 2.7.1.37) (GSK-3 BETA) - HOMO SAPIENS (HUMAN), 420 aa.	1.90E-226	3

255	cg43966621	451	AGAGGCGGGAA ATGGGGAGCCC ATA[C/A]CCAAAG CCAGCCAGCGG GGTTCCCC	C	A	Gly	Gly	SILENT-CODING	kinase	Human Gene SWISSPROT-ID:Q15119 [PYRUVATE DEHYDROGENASE(LIPOAMIDE)] KINASE ISOZYME 2 PRECURSOR (EC 2.7.1.99) (PYRUVATE DEHYDROGENASE KINASE ISOFORM 2) - HOMO SAPIENS (HUMAN), 407 aa.\|pcls:SPTREMBL-ID:Q15119 PYRUVATE DEHYDROGENASE KINASE - HOMO SAPIENS (HUMAN), 407 aa.	3.80E-219	17
256	cg38438124	346	CGACCCCCGGC AACCTAGGGTCC TC[T/C]GTCCTGG CGAGCAAGACCA AGACCA	T	C	Ser	Ser	SILENT-CODING	kinase	Human Gene SWISSNEW-ID:O70172 PHOSPHATIDYLINOSITOL-4-PHOSPHATE 5-KINASE TYPE II ALPHA (EC 2.7.1.68) (PIP5KII-ALPHA) (1-PHOSPHATIDYLINOSITOL-4-PHOSPHATE KINASE) (PTDINS(4)P-5-KINASE B ISOFORM) (DIPHOSPHOINOSITIDE KINASE) - MUS MUSCULUS (MOUSE), 405 aa.	2.80E-216	10
257	cg43917871	2435	AGTATTCTCGAG GTCTGTGTGTAT T[A/G]ACATCTGT GTAAACTCTGGC CCTGC	A	G	Val	Val	SILENT-CODING	kinase	Human Gene SWISSPROT-ID:P19138 CASEIN KINASE II, ALPHA CHAIN (CK II) (EC 2.7.1.37) - HOMO SAPIENS (HUMAN), AND BOS TAURUS (BOVINE), 391 aa.	2.00E-215	11 (20p13)
258	cg43924218	902	TTGCAGCAGTAG AGAAGAATGGTG G[C/A]TACAACCA ACTCTGTGATAT CTGGG	C	A	Gly	Gly	SILENT-CODING	kinase	Human Gene SPTREMBL-ID:Q12851 GC KINASE - HOMO SAPIENS (HUMAN), 819 aa.	1E-203	
259	cg43982923	940	TTGTAAAGTCAT TCCTCTTCCAGC T[A/T]CTAAAAGG GCTGGGATTCTG TCATA	A	T	Leu	Leu	SILENT-CODING	kinase	Human Gene SWISSPROT-ID:P49615 CELL DIVISION PROTEIN KINASE 5 (EC 2.7.1.-) (TAU PROTEIN KINASE II CATALYTIC SUBUNIT) (TPKII CATALYTIC SUBUNIT) (KINASE PSSALRE) (CRK6) - MUS MUSCULUS (MOUSE), 292 aa.	3.6E-159	19

260	cg43969473	3923	TCACCTGGCAAGCTCTCGGGGCACT[C/T]TGTCCGATAGTGAAATTGAGACCAA	C	T	Leu	Leu	SILENT-CODING	kinase	Human Gene SPTREMBL-ID:Q27467 SIMILARITY TO TYROSINE-PROTEIN KINASE - CAENORHABDITIS ELEGANS, 1280 aa.	2.1E-154	11
261	cg43958362	2164	GGCCACCATGCCGCTCCAGCGCGGC[G/C]CGCTCACTGCTGGTATTGCCCATGA	G	C	Arg	Arg	SILENT-CODING	kinase	Human Gene Homologous to TREMBLNEW-ID:E1253867 AMP-ACTIVATED PROTEIN KINASE, BETA 1 SUBUNIT - HOMO SAPIENS (HUMAN), 270 aa.	7.10E-147	12
262	cg42925992	327	TTGCAGTTGTGCAGCAAGAAATTAT[C/T]ATGATGAAAGACTGTAAACACCCAA	C	T	Ile	Ile	SILENT-CODING	kinase	Human Gene Homologous to SPTREMBL-ID:Q12851 GC KINASE - HOMO SAPIENS (HUMAN), 819 aa.	5.10E-105	
263	cg44033347	719	GGTGGATGCTGCTGTGCTGGCCCCC[G/A]TCTGCCCAGCTCACCAGCTCACTGC	G	A	Asp	Asp	SILENT-CODING	kinase	Human Gene Similar to SWISSPROT-ID:O00746 NUCLEOSIDE DIPHOSPHATE KINASE, MITOCHONDRIAL PRECURSOR (EC 2.7.4.6) (NDP KINASE, MITOCHONDRIAL) (NDK) (NM23-H4) - HOMO SAPIENS (HUMAN), 187 aa.\|pcls:SPTREMBL-ID:O00746 NUCLEOSIDE-DIPHOSPHATE KINASE (EC 2.7.4.6) (NUCLEOSIDE 5'-DIPHOSPHATE PHOSPHOTRANSFERASE) (NDK) - HOMO SAPIENS (HUMAN), 187 aa.	9.10E-99	16

264	cg43966625	337	CCGACCGAGTG CTGAGCACACCC TC[C/T]GTGCAGC TGGTGCAGAGCT GGTATG	C	T	Ser	Ser	SILENT-CODING	kinase	Human Gene Similar to SWISSPROT-ID:Q15119 [PYRUVATE DEHYDROGENASE(LIPOAMIDE)] KINASE ISOZYME 2 PRECURSOR (EC 2.7.1.99) (PYRUVATE DEHYDROGENASE KINASE ISOFORM 2) - HOMO SAPIENS (HUMAN), 407 aa.\|pcls:SPTREMBL-ID:Q15119 PYRUVATE DEHYDROGENASE KINASE - HOMO SAPIENS (HUMAN), 407 aa.	3.20E-89	17
265	cg43918784	1346	CTTCTTCTCTGT CTGCAACACACT G[A/G]TCAAAGAT TTCACCCCCAGC AGCAT	A	G	Asp	Asp	SILENT-CODING	kinase	Human Gene Similar to TREMBLNEW-ID:D1025880 ZIP-KINASE - HOMO SAPIENS (HUMAN), 454 aa.	1.80E-57	7
266	cg43933456	286	ATAGTAAGTTTT CATCAGTAGCTT C[T/C]TGTATAAG GTAATGCACATG TCCTT	T	C	Gln	Gln	SILENT-CODING	kinase	Human Gene Similar to SWISSPROT-ID:P35169 PHOSPHATIDYLINOSITOL 3-KINASE TOR1 (EC 2.7.1.137) (PI3-KINASE) (PTDINS-3-KINASE) (PI3K) - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 2470 aa.	2.10E-57	3
267	cg43105476	550	CCAGGAACTCCA CCACCCGGAGG TG[G/A]CCTTCTT TGGCAGCCAAGT GCAAGG	G	A	Gly	Gly	SILENT-CODING	kinaseinhibitor	Human Gene Similar to SWISSPROT-ID:P42773 CYCLIN-DEPENDENT KINASE 6 INHIBITOR (P18-INK6) - HOMO SAPIENS (HUMAN), 168 aa.	7.80E-86	
268	cg44931523	926	CCGTCATCTGGG CCACCAGGTCAA A[A/G]GATGCAAA CCCCGCACTGAC GAAGC	A	G	Ser	Ser	SILENT-CODING	kinasereceptor	Human Gene SWISSPROT-ID:P54753 EPHRIN TYPE-B RECEPTOR 3 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR HEK-2) - HOMO SAPIENS (HUMAN), 998 aa.	0.00E+00	3
269	cg43048869	2392	GTAACTTGGTGT GTAAGGTTTCTG A[C/T]TTCGGACT CTCGCGGGTACT GGAAG	C	T	Asp	Asp	SILENT-CODING	kinasereceptor	Human Gene SWISSPROT-ID:P29320 EPHRIN TYPE-A RECEPTOR 3 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR ETK1) (HEK) - HOMO SAPIENS (HUMAN), 983 aa.	0	

270	cg43935828	1884	AGGGCCGCCCC CTGCTCATGGTC TT[C/T]GAGTATA TGCGGCACGGG GACCTCA	C	T	Phe	Phe	SILENT-CODING	kinaserec eptor	Human Gene SWISSNEW-ID:P04629 HIGH AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (EC 2.7.1.112) (TRK1 TRANSFORMING TYROSINE KINASE PROTEIN) (P140-TRKA) (TRK-A) - HOMO SAPIENS (HUMAN), 796 aa.\|pcls:SWISSPROT-ID:P04629 HIGH AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (EC 2.7.1.112) (TRK1 TRANSFORMING TYROSINE KINASE PROTEIN) (P140-TRKA) (TRK-A) - HOMO SAPIENS (HUMAN), 796 aa.	0	
271	cg43935828	1935	ACCGCTTCCTCC GATCCCATGGAC C[C/T]GATGCCAA GCTGCTGGCTG GTGGGG	C	T	Pro	Pro	SILENT-CODING	kinaserec eptor	Human Gene SWISSNEW-ID:P04629 HIGH AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (EC 2.7.1.112) (TRK1 TRANSFORMING TYROSINE KINASE PROTEIN) (P140-TRKA) (TRK-A) - HOMO SAPIENS (HUMAN), 796 aa.\|pcls:SWISSPROT-ID:P04629 HIGH AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (EC 2.7.1.112) (TRK1 TRANSFORMING TYROSINE KINASE PROTEIN) (P140-TRKA) (TRK-A) - HOMO SAPIENS (HUMAN), 796 aa.	0	

272	cg43935828	2004	CCCTGGGTCTG GGGCAGCTGCT GGC[C/T]GTGGC TAGCCAGGTCGC TGCGGGGA	C	T	Ala	Ala	SILENT-CODING	kinaserec eptor	Human Gene SWISSNEW-ID:P04629 HIGH AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (EC 2.7.1.112) (TRK1 TRANSFORMING TYROSINE KINASE PROTEIN) (P140-TRKA) (TRK-A) - HOMO SAPIENS (HUMAN), 796 aa.\|pcls:SWISSPROT-ID:P04629 HIGH AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (EC 2.7.1.112) (TRK1 TRANSFORMING TYROSINE KINASE PROTEIN) (P140-TRKA) (TRK-A) - HOMO SAPIENS (HUMAN), 796 aa.	0	
273	cg43991478	1342	CGTCAGCAAGAT TGTGGGGCTGC AG[C/G]CGGGTG AGGTCACGCAG GATGGTGC	C	G	Arg	Arg	SILENT-CODING	kinaserec eptor	Human Gene SWISSPROT-ID:P29597 NON-RECEPTOR TYROSINE-PROTEIN KINASE TYK2 (EC 2.7.1.112) - HOMO SAPIENS (HUMAN), 1187 aa.	0	
274	cg43263845	668	GTAATGAAAAGT TTTCTTATTTTCC [G/A]GAGATGGA AGTCACACAGCC CACTT	G	A	Pro	Pro	SILENT-CODING	kinaserec eptor	Human Gene TREMBLNEW-ID:G247985 ACTIVIN RECEPTOR, ACTRIIB=TRANSMEMBRANE PROTEIN SERINE KINASE - XENOPUS LAEVIS, 510 aa.	3.30E-204	2
275	cg43999555	1415	GCGGATCGTGG AGAACCTGGGCA TC[C/T]TGACCGG GCCGCAGCTCTT CTCCCT	C	T	Leu	Leu	SILENT-CODING	kinaserec eptor	Human Gene Similar to SWISSPROT-ID:Q12929 EPIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE EPS8 - HOMO SAPIENS (HUMAN), 822 aa.\|pcls:SPTREMBL-ID:Q12929 EPIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE - HOMO SAPIENS (HUMAN), 822 aa.	1.20E-99	11
276	cg43975720	5392	CCTCTCCTGCCA GACAGCCCACG AC[C/T]GGGTCG ACCCCCCAGGG GACGCCCA	C	T	Thr	Thr	SILENT-CODING	kinesin	Human Gene SWISSPROT-ID:Q12756 KINESIN-LIKE PROTEIN KIF1A (AXONAL TRANSPORTER OF SYNAPTIC VESICLES) - HOMO SAPIENS (HUMAN), 1690 aa.	0.00E+00	2

277	cg43987378	967	CAGCCCTGTCAAGCAGCCAAGCAGA[G/A]GTGGCATCTCTGCGGCAGGAGACTG	G	A	Glu	Glu	SILENT-CODING	kinesin	Human Gene SPTREMBL-ID:Q14834 KINESIN-RELATED PROTEIN - HOMO SAPIENS (HUMAN), 519 aa (fragment).	1.50E-254	6
278	cg44009224	123	GCTACAGTTCACAGCAGCAAAGGGT[A/G]CCATTTCTTCAGCCTCCCGGTCAAA	A	G	Val	Val	SILENT-CODING	laminin	Human Gene SWISSPROT-ID:Q16787 LAMININ ALPHA-3 CHAIN PRECURSOR (EPILIGRIN 170 KD SUBUNIT) (E170) - HOMO SAPIENS (HUMAN), 1713 aa.	0.00E+00	
279	cg42488873	988	CATGCACGTCCTCAAGGCTGTACCC[C/T]AGCTGCGTCGACAGTGCTTGTATTA	C	T	Leu	Leu	SILENT-CODING	lipase	Human Gene SWISSPROT-ID:P54317 PANCREATIC LIPASE RELATED PROTEIN 2 PRECURSOR (EC 3.1.1.3) - HOMO SAPIENS (HUMAN), 469 aa.	9.80E-261	
280	cg42488873	202	GATTTATCCCACGTTTGTTCCAGAG[A/G]AATTTAACTTTCTGTATTTTTCCAA	A	G	Phe	Phe	SILENT-CODING	lipase	Human Gene SWISSPROT-ID:P54317 PANCREATIC LIPASE RELATED PROTEIN 2 PRECURSOR (EC 3.1.1.3) - HOMO SAPIENS (HUMAN), 469 aa.	9.80E-261	
281	cg42686658	452	ACTTTGCCCGCTTTGACCCGCAGGG[C/T]GGGCTGGCCGGCATCGCCGCAATCA	C	T	Gly	Gly	SILENT-CODING	MHC	Human Gene Homologous to SWISSPROT-ID:P06340 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DZ ALPHA CHAIN PRECURSOR (MHC DN-ALPHA) - HOMO SAPIENS (HUMAN), 250 aa.	3.70E-134	6 (6p21.3)
282	cg42686658	860	CACCAGATGCCATGGAGACCCTGGT[C/T]TGTGCCCTGGGCCTGGCCATCGGCC	C	T	Val	Val	SILENT-CODING	MHC	Human Gene Homologous to SWISSPROT-ID:P06340 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DZ ALPHA CHAIN PRECURSOR (MHC DN-ALPHA) - HOMO SAPIENS (HUMAN), 250 aa.	3.7E-134	6 (6p21.3)
283	cg42928872	389	TGAGCCTAGACCCGCGCGTCTCCAT[C/T]TACAGCACGCGCCGCCCGGTGTTGG	C	T	Ile	Ile	SILENT-CODING	misc_channel	Human Gene TREMBLNEW-ID:G2465531 KIDNEY AND CARDIAC VOLTAGE DEPENDENT K+ CHANNEL - HOMO SAPIENS (HUMAN), 676 aa.	0	11

284	cg43311602	5361	CTCGCCCCGCC GGCTACCCCAG CAC[A/G]GTCAG CACTGTGGAGG GCCACGGGC	A	G	Thr	Thr	SILENT-CODING	misc_channel	Human Gene SPTREMBL-ID:Q13930 VOLTAGE-DEPENDENT L-TYPE CA CHANNEL ALPHA 1 SUBUNIT - HOMO SAPIENS (HUMAN), 2173 aa.	0	12 (12p13.3)
285	cg43111577	175	TGGAACCAGAGC CAGAGATGGAG GC[A/G]GAGGTG GAACCAGAACCG AATCCTG	A	G	Ala	Ala	SILENT-CODING	misc_channel	Human Gene TREMBLNEW-ID:G1518639 CGMP-GATED CATION CHANNEL BETA SUBUNIT - HOMO SAPIENS (HUMAN), 1251 aa.	0	16 (16q13)
286	cg21657051	5819	AAGGCATGAGG GTGGTTGTGAAT GC[C/T]CTTGTTA GGAGCAATTCCC TCTATC	C	T	Ala	Ala	SILENT-CODING	misc_channel	Human Gene TREMBLNEW-ID:G2665784 VOLTAGE-GATED SODIUM CHANNEL, SUBTYPE III - HOMO SAPIENS (HUMAN), 1366 aa (fragment).	0	
287	cg42684570	1186	CCGAGTAGCCCA GGAGGAGTGTAA T[C/T]TTGAAAGA GACCCTCTCGCC ACTGT	C	T	Lys	Lys	SILENT-CODING	misc_channel	Human Gene SWISSPROT-ID:P46098 5-HYDROXYTRYPTAMINE 3 RECEPTOR PRECURSOR (5-HT-3) (SEROTONIN-GATED ION CHANNEL RECEPTOR) - HOMO SAPIENS (HUMAN), 478 aa.	1.8E-260	11 (11q23.1)
288	cg44021559	2938	TCCTGTCATTAG GGATGACGTGG GT[A/G]CCATTGT AGATGCCCACTT GCACCA	A	G	Gly	Gly	SILENT-CODING	misc_channel	Human Gene Similar to SPTREMBL-ID:Q61626 GLUTAMATE RECEPTOR CHANNEL SUBUNIT GAMMA 2 PRECURSOR - MUS MUSCULUS (MOUSE), 979 aa.	2E-61	9 (9q34.3)
289	cg44021559	2989	GCTTGCGGTTCT GCAGGTTCATGA T[A/G]CTATAGTT GGCGAACTTCCG GTCCC	A	G	Ser	Ser	SILENT-CODING	misc_channel	Human Gene Similar to SPTREMBL-ID:Q61626 GLUTAMATE RECEPTOR CHANNEL SUBUNIT GAMMA 2 PRECURSOR - MUS MUSCULUS (MOUSE), 979 aa.	2E-61	9 (9q34.3)
290	cg44021559	2992	TGCGGTTCTGCA GGTTCATGATAC T[A/G]TAGTTGGC GAACTTCCGGTC CCCAT	A	G	Tyr	Tyr	SILENT-CODING	misc_channel	Human Gene Similar to SPTREMBL-ID:Q61626 GLUTAMATE RECEPTOR CHANNEL SUBUNIT GAMMA 2 PRECURSOR - MUS MUSCULUS (MOUSE), 979 aa.	2E-61	9 (9q34.3)

291	cg44929972	1029	AAAAGCTTGAGA TGCATTTCCATA A[G/A]CTTCCAAG CCTCCTCTCTTG TGATG	G	A	Lys	Lys	SILENT-CODING	ngf	Human Gene TREMBLNEW-ID:E1216872 NERVE GROWTH FACTOR-INDUCIBLE PC4 HOMOLOGUE - HOMO SAPIENS (HUMAN), 453 aa.	4.7E-214	7
292	cg44929972	1044	ATTTCCATAAGC TTCCAAGCCTCC T[C/T]TCTTGTGA TGATGTAAACAT GAGAA	C	T	Leu	Leu	SILENT-CODING	ngf	Human Gene TREMBLNEW-ID:E1216872 NERVE GROWTH FACTOR-INDUCIBLE PC4 HOMOLOGUE - HOMO SAPIENS (HUMAN), 453 aa.	4.7E-214	7
293	cg44929972	1071	CTTGTGATGATG TAAACATGAGAA T[A/T]GCTGCTGG TGAATCTTTGGC ACTTC	A	T	Ile	Ile	SILENT-CODING	ngf	Human Gene TREMBLNEW-ID:E1216872 NERVE GROWTH FACTOR-INDUCIBLE PC4 HOMOLOGUE - HOMO SAPIENS (HUMAN), 453 aa.	4.7E-214	7
294	cg44929972	1080	ATGTAAACATGA GAATAGCTGCTG G[T/C]GAATCTTT GGCACTTCTCTT TGAAT	T	C	Gly	Gly	SILENT-CODING	ngf	Human Gene TREMBLNEW-ID:E1216872 NERVE GROWTH FACTOR-INDUCIBLE PC4 HOMOLOGUE - HOMO SAPIENS (HUMAN), 453 aa.	4.7E-214	7
295	cg44929972	1098	CTGCTGGTGAAT CTTTGGCACTTC T[C/G]TTTGAATT GGCCAGAGGAA TAGAGA	C	G	Leu	Leu	SILENT-CODING	ngf	Human Gene TREMBLNEW-ID:E1216872 NERVE GROWTH FACTOR-INDUCIBLE PC4 HOMOLOGUE - HOMO SAPIENS (HUMAN), 453 aa.	4.7E-214	7
296	cg44929972	1143	TAGAGAGTGACT TTTTTTATGAAGA [C/T]ATGGAGTCC TTGACGCAGATG CTTA	C	T	Asp	Asp	SILENT-CODING	ngf	Human Gene TREMBLNEW-ID:E1216872 NERVE GROWTH FACTOR-INDUCIBLE PC4 HOMOLOGUE - HOMO SAPIENS (HUMAN), 453 aa.	4.7E-214	7
297	cg44929972	1158	TTTATGAAGACA TGGAGTCCTTGA C[G/C]CAGATGC TTAGGGCCTTGG CAACAG	G	C	Thr	Thr	SILENT-CODING	ngf	Human Gene TREMBLNEW-ID:E1216872 NERVE GROWTH FACTOR-INDUCIBLE PC4 HOMOLOGUE - HOMO SAPIENS (HUMAN), 453 aa.	4.7E-214	7

298	cg44929972	1167	ACATGGAGTCCT TGACGCAGATGC T[T/C]AGGGCCTT GGCAACAGATG GAAATA	T	C	Leu	Leu	SILENT-CODING	ngf	Human Gene TREMBLNEW-ID:E1216872 NERVE GROWTH FACTOR-INDUCIBLE PC4 HOMOLOGUE - HOMO SAPIENS (HUMAN), 453 aa.	4.7E-214	7
299	cg44929972	1173	AGTCCTTGACGC AGATGCTTAGGG C[C/T]TTGGCAAC AGATGGAAATAA ACACC	C	T	Ala	Ala	SILENT-CODING	ngf	Human Gene TREMBLNEW-ID:E1216872 NERVE GROWTH FACTOR-INDUCIBLE PC4 HOMOLOGUE - HOMO SAPIENS (HUMAN), 453 aa.	4.7E-214	7
300	cg44929972	1179	TGACGCAGATGC TTAGGGCCTTGG C[A/T]ACAGATGG AAATAAACACCG GGCCA	A	T	Ala	Ala	SILENT-CODING	ngf	Human Gene TREMBLNEW-ID:E1216872 NERVE GROWTH FACTOR-INDUCIBLE PC4 HOMOLOGUE - HOMO SAPIENS (HUMAN), 453 aa.	4.7E-214	7
301	cg44929972	1230	AAGTGGACAAGA GAAAGCAGCGG TC[A/T]GTTTTCA GAGATGTCCTGA GGGCAG	A	T	Ser	Ser	SILENT-CODING	ngf	Human Gene TREMBLNEW-ID:E1216872 NERVE GROWTH FACTOR-INDUCIBLE PC4 HOMOLOGUE - HOMO SAPIENS (HUMAN), 453 aa.	4.7E-214	7
302	cg44929972	1242	GAAAGCAGCGG TCAGTTTTCAGA GA[T/C]GTCCTGA GGGCAGTGGAG GAACGGG	T	C	Asp	Asp	SILENT-CODING	ngf	Human Gene TREMBLNEW-ID:E1216872 NERVE GROWTH FACTOR-INDUCIBLE PC4 HOMOLOGUE - HOMO SAPIENS (HUMAN), 453 aa.	4.7E-214	7
303	cg44929972	1245	AGCAGCGGTCA GTTTTCAGAGAT GT[C/T]CTGAGG GCAGTGGAGGA ACGGGATT	C	T	Val	Val	SILENT-CODING	ngf	Human Gene TREMBLNEW-ID:E1216872 NERVE GROWTH FACTOR-INDUCIBLE PC4 HOMOLOGUE - HOMO SAPIENS (HUMAN), 453 aa.	4.7E-214	7
304	cg43921419	1269	GTGGAGATCCTT TTAGTGCAGATG A[C/T]ATACTTTT TCCTGTCCTTCA GTCCC	C	T	Asp	Asp	SILENT-CODING	nucl_rec pt	Human Gene SPTREMBL-ID:Q14452 GLUCOCORTICOID RECEPTOR REPRESSION FACTOR 1 - HOMO SAPIENS (HUMAN), 835 aa.	0	19

305	cg43249083	633	CGCTCTCAGCTG GTGAAGACATGA C[G/C]ACCCTGG ACTCCAACAACA ACACAG	G	C	Thr	Thr	SILENT-CODING	nucl_rec pt	Human Gene SWISSPROT-ID:P20393 V-ERBA RELATED PROTEIN EAR-1 - HOMO SAPIENS (HUMAN), 614 aa.	0	17 (17q11.2)
306	cg43315956	2680	TCAGGAATGACA GGAACAAGAAAA A[G/A]AAGGAGA CTTCGAAGCAAG AATGCA	G	A	Lys	Lys	SILENT-CODING	nucl_rec pt	Human Gene SWISSPROT-ID:P10826 RETINOIC ACID RECEPTOR BETA-2 (RAR-BETA-2) (RAR-EPSILON) - HOMO SAPIENS (HUMAN), 448 aa.	2.3E-244	3
307	cg43935583	1416	TGGGAGGGGGC ATGCCTGGAATG GC[T/C]GGAATG CCTGGACTCAAT GAAATTC	T	C	Ala	Ala	SILENT-CODING	nucl_rec pt	Human Gene SWISSPROT-ID:P50502 HSC70-INTERACTING PROTEIN (PROGESTERONE RECEPTOR-ASSOCIATED P48 PROTEIN) - HOMO SAPIENS (HUMAN), 369 aa.	1.3E-195	22
308	cg43935583	1563	AGAGCAACCCAA AGGTTATGAATC T[C/T]ATCAGTAA ATTGTCAGCCAA ATTTG	C	T	Leu	Leu	SILENT-CODING	nucl_rec pt	Human Gene SWISSPROT-ID:P50502 HSC70-INTERACTING PROTEIN (PROGESTERONE RECEPTOR-ASSOCIATED P48 PROTEIN) - HOMO SAPIENS (HUMAN), 369 aa.	1.30E-195	22
309	cg42933659	233	TACTCTGTATTAA CTCTTCCTTTGA[G/A]AGTTTTGAA GGTGAAGCATTT TGAT	G	A	Leu	Leu	SILENT-CODING	nucl_rec pt	Human Gene Similar to SPTREMBL-ID:Q60974 NUCLEAR RECEPTOR CO-REPRESSOR - MUS MUSCULUS (MOUSE), 2453 aa.	2.20E-51	17
310	cg44926604	827	CTCACAGCTGCT CAAATGGGAACA G[A/G]TGGGAAG CTGCTGCTTTCT TTTCCC	A	G	His	His	SILENT-CODING	nuclease	Human Gene SWISSPROT-ID:Q01831 DNA-REPAIR PROTEIN COMPLEMENTING XP-C CELLS (XERODERMA PIGMENTOSUM GROUP C COMPLEMENTING PROTEIN) (P125) HOMO SAPIENS (HUMAN), 939 aa.	0.00E+00	3

311	cg44128653	1448	CGTAGGTACAGGCGCTATGAGGCCA[G/A]CTGTATGCAGCAGAGGAGGCCGGTG	G	A	Ser	Ser	SILENT-CODING	nuclease	Human Gene SWISSNEW-ID:O00115 DEOXYRIBONUCLEASE II PRECURSOR (EC 3.1.22.1) (DNASE II) (ACID DNASE) (LYSOSOMAL DNASE II) (R31240_2) - HOMO SAPIENS (HUMAN), 360 aa.\|pcls:SWISSPROT-ID:O00115 DEOXYRIBONUCLEASE II PRECURSOR (EC 3.1.22.1) (DNASE II) (ACID DNASE) (LYSOSOMAL DNASE II) (R31240_2) - HOMO SAPIENS (HUMAN), 360 aa.	1.40E-203	19
312	cg43952559	211	GAATGTTAACTGACTTAAGAGCCAT[T/C]AATTCAGTTATACAACCTATGGGAG	T	C	Ile	Ile	SILENT-CODING	nuclease	Human Gene SWISSNEW-ID:P10266 RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE] - HOMO SAPIENS (HUMAN), 874 aa.\|pcls:SWISSPROT-ID:P10266 RETROVIRUS-RELATED POL POLYPROTEIN (REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE) - HOMO SAPIENS (HUMAN), 874 aa.	7.80E-156	
313	cg43952559	235	TTAATTCAGTTATACAACCTATGGG[A/G]GCATTACAGCCAGGATTGCCTTCTC	A	G	Gly	Gly	SILENT-CODING	nuclease	Human Gene SWISSNEW-ID:P10266 RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE] - HOMO SAPIENS (HUMAN), 874 aa.\|pcls:SWISSPROT-ID:P10266 RETROVIRUS-RELATED POL POLYPROTEIN (REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE) - HOMO SAPIENS (HUMAN), 874 aa.	7.80E-156	

314	cg43952559	251	ACCTATGGGAGCATTACAGCCAGGA[T/C]TGCCTTCTCCTGCTATGATTCCAAA	T	C	Leu	Leu	SILENT-CODING	nuclease	Human Gene SWISSNEW-ID:P10266 RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE] - HOMO SAPIENS (HUMAN), 874 aa.\|pcls:SWISSPROT-ID:P10266 RETROVIRUS-RELATED POL POLYPROTEIN (REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE) - HOMO SAPIENS (HUMAN), 874 aa.	7.80E-156	
315	cg43952559	884	TAACAAAGGAGGCGGAGGCAGAGTT[A/G]CAACTGATCGAGAAGCAAGTCCATA	A	G	Leu	Leu	SILENT-CODING	nuclease	Human Gene SWISSNEW-ID:P10266 RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE] - HOMO SAPIENS (HUMAN), 874 aa.\|pcls:SWISSPROT-ID:P10266 RETROVIRUS-RELATED POL POLYPROTEIN (REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE) - HOMO SAPIENS (HUMAN), 874 aa.	7.80E-156	
316	cg43952559	896	CGGAGGCAGAGTTACAACTGATCGA[G/A]AAGCAAGTCCATAAAGCTCAAATAA	G	A	Glu	Glu	SILENT-CODING	nuclease	Human Gene SWISSNEW-ID:P10266 RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE] - HOMO SAPIENS (HUMAN), 874 aa.\|pcls:SWISSPROT-ID:P10266 RETROVIRUS-RELATED POL POLYPROTEIN (REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE) - HOMO SAPIENS (HUMAN), 874 aa.	7.80E-156	

317	cg43952559	914	TGATCGAGAAGC AAGTCCATAAAG C[T/C]CAAATAAA TAGAATAGATCC AGAGA	T	C	Ala	Ala	SILENT-CODING	nuclease	Human Gene SWISSNEW-ID:P10266 RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE] - HOMO SAPIENS (HUMAN), 874 aa.\|pcls:SWISSPROT-ID:P10266 RETROVIRUS-RELATED POL POLYPROTEIN (REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE) - HOMO SAPIENS (HUMAN), 874 aa.	7.80E-156	
318	cg43943773	407	TATTGAGTTCAT CATTAAAGTCAT C[T/G]ATTTTCAA CCTGAGTGTCCG GAGGG	T	G	Ile	Ile	SILENT-CODING	nucleasei nhib	Human Gene Similar to SWISSPROT-ID:P29315 RIBONUCLEASE INHIBITOR RATTUS NORVEGICUS (RAT), 456 aa.	1.30E-51	19
319	cg43943851	851	TTGTAACTGTGA ACTGTGCCCGG CT[G/C]CTGAAAG CCGACCACCATG CAACCA	G	C	Leu	Leu	SILENT-CODING	oncogen e	Human Gene SWISSPROT-ID:Q15582 TRANSFORMING GROWTH FACTOR-BETA INDUCED PROTEIN IG-H3 PRECURSOR (BETA IG-H3) (KERATO-EPITHELIN) - HOMO SAPIENS (HUMAN), 683 aa.	0.00E+00	5 (5q31)
320	cg44012756	2265	GGACCAACTGTG ACATCAACAACA A[T/C]GAGTGTGA ATCCAACCCTTG TGTCA	T	C	Asn	Asn	SILENT-CODING	oncogen e	Human Gene SWISSPROT-ID:P31695 NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 4 PRECURSOR (TRANSFORMING PROTEIN INT-3) - MUS MUSCULUS (MOUSE), 1964 aa.	0.00E+00	
321	cg42827675	215	CAGCCCCGGGC ATGTTCCGAGAC TT[C/T]GGGGAAC CCGGCCCGAGC TCCGGGA	C	T	Phe	Phe	SILENT-CODING	oncogen e	Human Gene Homologous to SWISSPROT-ID:P15407 FOS-RELATED ANTIGEN 1 - HOMO SAPIENS (HUMAN), 271 aa.	6.40E-146	11

322	cg43964295	4723	TATCACAGTACA GGCCTTGCCAG CC[G/A]TACTGG CACCTGCAGTCA CCTGGGA	G	A	Tyr	Tyr	SILENT-CODING	oncogene	Human Gene Homologous to SWISSPROT-ID:P31695 NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 4 PRECURSOR (TRANSFORMING PROTEIN INT-3) - MUS MUSCULUS (MOUSE), 1964 aa.	4.80E-120	20
323	cg43916615	130	TGACCATCCAGC TGATCCAGAACC A[C/T]TTTGTGGA CGAATACGACCC CACTA	C	T	His	His	SILENT-CODING	oncogene	Human Gene Similar to TREMBLNEW-ID:G332185 TRANSFORMING PROTEIN (P21 HAS) - HARVEY MURINE SARCOMA VIRUS, 241 aa.	3.10E-98	
324	cg42904626	640	AACATAAAGAAA AGATGAGCAAAG A[C/T]GGTAAAAA GAAGAAAAAGAA GTCAA	C	T	Asp	Asp	SILENT-CODING	oncogene	Human Gene Similar to SWISSPROT-ID:P01118 TRANSFORMING PROTEIN P21/K-RAS 2B - HOMO SAPIENS (HUMAN), 188 aa.	1.1E-97	12
325	cg44029157	533	GCTTCCTGCTGG TGTTCGCCATTA A[T/C]GACCGGC AGAGTTTCAACG AGGTGG	T	C	Asn	Asn	SILENT-CODING	oncogene	Human Gene Similar to SWISSPROT-ID:P17082 RAS-RELATED PROTEIN R-RAS2 (RAS-LIKE PROTEIN TC21) (TERATOCARCINOMA ONCOGENE) - HOMO SAPIENS (HUMAN), 204 aa.	5.1E-66	
326	cg43975131	4247	TCTTCTTCTTCA GGCGCTCGATG GC[C/A]CGGCTC TGGCCTTTGTTG GCTTTCT	C	A	Arg	Arg	SILENT-CODING	oncogene	Human Gene Similar to SPTREMBL-ID:Q13692 BCR/ABL FUSION PROTEIN HOMO SAPIENS (HUMAN), 284 aa (fragment).	1.8E-64	17 (17p13.3)
327	cg43307658	1322	CCGGCTTCGAG CAGGCCTACCCT GA[T/C]CCCGGT CCCGAGGCGGC GCAGGCCC	T	C	Asp	Asp	SILENT-CODING	oxidase	Human Gene SPTREMBL-ID:Q08397 PROTEIN-LYSINE OXIDASE HOMOLOG PRECURSOR (EC 1.4.3.13) (LYSYL OXIDASE HOMOLOG) (LYSYL OXIDASE-LIKE PROTEIN) - HOMO SAPIENS (HUMAN), 574 aa.	0	15

328	cg43307658	1514	GCGCGCAGCAG GGCCGCCTCAG CGT[G/A]GGCAG CGTGTACCGGC CCAACCAGA	G	A	Val	Val	SILENT-CODING	oxidase	Human Gene SPTREMBL-ID:Q08397 PROTEIN-LYSINE OXIDASE HOMOLOG PRECURSOR (EC 1.4.3.13) (LYSYL OXIDASE HOMOLOG) (LYSYL OXIDASE-LIKE PROTEIN) - HOMO SAPIENS (HUMAN), 574 aa.	0	15
329	cg44028217	1031	GCACCAGCACCT GGCCCTTCAGCC C[C/T]GCATAGAA GTTGAAGCCACC TTTAA	C	T	Ala	Ala	SILENT-CODING	oxidase	Human Gene SWISSPROT-ID:P19801 AMILORIDE-SENSITIVE AMINE OXIDASE (COPPER-CONTAINING) PRECURSOR (EC 1.4.3.6) (DIAMINE OXIDASE) (DAO) (AMILORIDE-BINDING PROTEIN) (ABP) (HISTAMINASE) - HOMO SAPIENS (HUMAN), 751 aa.	0.00E+00	7 (7q31)
330	cg44028217	471	GGTAGATGCTGC TGCTGCACAGCT C[C/T]GACTCCC GGTACTTGGTCA CTGCCA	C	T	Ser	Ser	SILENT-CODING	oxidase	Human Gene SWISSPROT-ID:P19801 AMILORIDE-SENSITIVE AMINE OXIDASE (COPPER-CONTAINING) PRECURSOR (EC 1.4.3.6) (DIAMINE OXIDASE) (DAO) (AMILORIDE-BINDING PROTEIN) (ABP) (HISTAMINASE) - HOMO SAPIENS (HUMAN), 751 aa.	0.00E+00	7 (7q31)
331	cg44028217	638	GGGGGCTGGTA AAGAGCAGGTAC TT[A/G]GGCAGCT TCCTTTTGAAGC GGAAGG	A	G	Pro	Pro	SILENT-CODING	oxidase	Human Gene SWISSPROT-ID:P19801 AMILORIDE-SENSITIVE AMINE OXIDASE (COPPER-CONTAINING) PRECURSOR (EC 1.4.3.6) (DIAMINE OXIDASE) (DAO) (AMILORIDE-BINDING PROTEIN) (ABP) (HISTAMINASE) - HOMO SAPIENS (HUMAN), 751 aa.	0.00E+00	7 (7q31)

332	cg44028217	725	GAGTTGGCTGGACCACGCGGTGTCT[T/C]GGGCTCCAGGGGTTGGTGATGTTTT	T	C	Pro	Pro	SILENT-CODING	oxidase	Human Gene SWISSPROT-ID:P19801 AMILORIDE-SENSITIVE AMINE OXIDASE (COPPER-CONTAINING) PRECURSOR (EC 1.4.3.6) (DIAMINE OXIDASE) (DAO) (AMILORIDE-BINDING PROTEIN) (ABP) (HISTAMINASE) - HOMO SAPIENS (HUMAN), 751 aa.	0.00E+00	7 (7q31)
333	cg43271573	1320	GGGCTGTTCGAGTCCTGAAAGGTGT[A/G]AATAAGTTACCACCACCAAGTGTCA	A	G	Val	Val	SILENT-CODING	oxidase	Human Gene SWISSPROT-ID:Q01740 DIMETHYLANILINE MONOOXYGENASE (N-OXIDE FORMING) 1 (EC 1.14.13.8) (FETAL HEPATIC FLAVIN-CONTAINING MONOOXYGENASE 1) (FMO 1) (DIMETHYLANILINE OXIDASE 1) - HOMO SAPIENS (HUMAN), 531 aa.	5.30E-293	1 (1q23)
334	cg43051423	618	ATCGCAGGTAGTGATAGCCTGAGGA[T/A]CCCCCAGTGCCAGCCTTGCTGCCTA	T	A	Gly	Gly	SILENT-CODING	oxygenase	Human Gene SWISSPROT-ID:P48775 TRYPTOPHAN 2,3-DIOXYGENASE (EC 1.13.11.11) (TRYPTOPHAN PYRROLASE) (TRYPTOPHANASE) (TRYPTOPHAN OXYGENASE) (TRYPTAMIN 2,3-DIOXYGENASE) (TRPO) - HOMO SAPIENS (HUMAN), 406 aa.	9.80E-221	4
335	cg43051423	633	AGCCTGAGGATCCCCCAGTGCCAGC[C/T]TTGCTGCCTAGCATCCTGTGCACCA	C	T	Lys	Lys	SILENT-CODING	oxygenase	Human Gene SWISSPROT-ID:P48775 TRYPTOPHAN 2,3-DIOXYGENASE (EC 1.13.11.11) (TRYPTOPHAN PYRROLASE) (TRYPTOPHANASE) (TRYPTOPHAN OXYGENASE) (TRYPTAMIN 2,3-DIOXYGENASE) (TRPO) - HOMO SAPIENS (HUMAN), 406 aa.	9.80E-221	4

336	cg43051423	642	ATCCCCCAGTGCCAGCCTTGCTGCC[T/C]AGCATCCTGTGCACCATGCACACAT	T	C	Leu	Leu	SILENT-CODING	oxygenase	Human Gene SWISSPROT-ID:P48775 TRYPTOPHAN 2,3-DIOXYGENASE (EC 1.13.11.11) (TRYPTOPHAN PYRROLASE) (TRYPTOPHANASE) (TRYPTOPHAN OXYGENASE) (TRYPTAMIN 2,3-DIOXYGENASE) (TRPO) - HOMO SAPIENS (HUMAN), 406 aa.	9.80E-221	4
337	cg43051423	648	CAGTGCCAGCCTTGCTGCCTAGCAT[C/T]CTGTGCACCATGCACACATGGTTAT	C	T	Arg	Arg	SILENT-CODING	oxygenase	Human Gene SWISSPROT-ID:P48775 TRYPTOPHAN 2,3-DIOXYGENASE (EC 1.13.11.11) (TRYPTOPHAN PYRROLASE) (TRYPTOPHANASE) (TRYPTOPHAN OXYGENASE) (TRYPTAMIN 2,3-DIOXYGENASE) (TRPO) - HOMO SAPIENS (HUMAN), 406 aa.	9.80E-221	4
338	cg43972840	190	ACCAAATGAGAATGGCTGACCTCTC[G/A]GAGCTCCTGAAGGAAGGGACCAAGG	G	A	Ser	Ser	SILENT-CODING	oxygenase	Human Gene SWISSPROT-ID:P30519 HEME OXYGENASE 2 (EC 1.14.99.3) (HO-2) - HOMO SAPIENS (HUMAN), 316 aa.	4.60E-168	16 (16p13.3)
339	cg43254736	905	AGCAGTTGGTGTGCAGGTAGTTGAA[A/G]TCGGACATGCCTCCCGTGAAGCTGT	A	G	Asp	Asp	SILENT-CODING	peptidase	Human Gene Similar to SPTREMBL-ID:P91359 SIMILARITY TO THE M14 PEPTIDASE FAMILY - CAENORHABDITIS ELEGANS, 985 aa.	1.10E-67	
340	cg41626506	1029	TGCTGTCACAAGACTCAAAGTCTTC[G/A]GGGAATTTGCCGACTTGGAAGGCAT	G	A	Pro	Pro	SILENT-CODING	peroxidase	Human Gene SWISSPROT-ID:P07202 THYROID PEROXIDASE PRECURSOR (EC 1.11.1.8) (TPO) - HOMO SAPIENS (HUMAN), 933 aa.	0.00E+00	3 (3q26.3)
341	cg41626506	1176	TGTTCTCCCACCAAAACCAGTCACC[G/A]TCCCGCAGAGCCTTCATCTGCTTCC	G	A	Asp	Asp	SILENT-CODING	peroxidase	Human Gene SWISSPROT-ID:P07202 THYROID PEROXIDASE PRECURSOR (EC 1.11.1.8) (TPO) - HOMO SAPIENS (HUMAN), 933 aa.	0.00E+00	3 (3q26.3)

342	cg40084915	1911	GGACGTCCATGCTGCGGTTCTTGTC[G/A]CGGTTCCGGGGCAACAGGGCGATGC	G	A	Arg	Arg	SILENT-CODING	phosphatase	Human Gene SPTREMBL-ID:O00197 RECEPTOR PROTEIN TYROSINE PHOSPHATASE HPTP-J PRECURSOR - HOMO SAPIENS (HUMAN), 1436 aa.	0.00E+00	1
343	cg43956369	4272	CAGTCTGGGGAGGTCCAGCCACTGG[G/A]ACTGCAGGATCAAATGATCTTATAC	G	A	Val	Val	SILENT-CODING	phosphatase	Human Gene SWISSNEW-ID:Q15262 PROTEIN-TYROSINE PHOSPHATASE KAPPA PRECURSOR (EC 3.1.3.48) (R-PTP- KAPPA) - HOMO SAPIENS (HUMAN), 1439 aa.\|pcls:SWISSPROT-ID:Q15262 PROTEIN-TYROSINE PHOSPHATASE KAPPA PRECURSOR (EC 3.1.3.48) (R-PTP- KAPPA) - HOMO SAPIENS (HUMAN), 1439 aa.	0.00E+00	6
344	cg43917453	3092	CGAGAACCTCCACGTCAGCGAACGC[A/G]CTGCTGGGCACCTGCAGGAGGCGGG	A	G	Ser	Ser	SILENT-CODING	phosphatase	Human Gene TREMBLNEW-ID:G2262075 IAR/RECEPTOR-LIKE PROTEIN-TYROSINE PHOSPHATASE PRECURSOR - HOMO SAPIENS (HUMAN), 1015 aa.	0.00E+00	7
345	cg43920534	4634	TTTTGTTTCTTTTGCAACTCTTCTA[G/A]ATATCCCAAAATGTCTTCATCTGCT	G	A	Leu	Leu	SILENT-CODING	phosphatase	Human Gene SPTREMBL-ID:Q10728 SERINE/THREONINE PROTEIN PHOSPHATASE PP1 SMOOTH MUSCLE REGULATORY M110 SUBUNIT (110 KDA SUBUNIT) - RATTUS NORVEGICUS (RAT), 976 aa.	0.00E+00	12
346	cg43920534	4641	TCTTTTGCAACTCTTCTAGATATCC[C/T]AAAATGTCTTCATCTGCTACATCAA	C	T	Leu	Leu	SILENT-CODING	phosphatase	Human Gene SPTREMBL-ID:Q10728 SERINE/THREONINE PROTEIN PHOSPHATASE PP1 SMOOTH MUSCLE REGULATORY M110 SUBUNIT (110 KDA SUBUNIT) - RATTUS NORVEGICUS (RAT), 976 aa.	0.00E+00	12
347	cg43920534	4749	TCCAACATGCTTCTTCTTTACCCCA[G/A]TGAGCTGCAGCATGAAGAGGTGTCC	G	A	His	His	SILENT-CODING	phosphatase	Human Gene SPTREMBL-ID:Q10728 SERINE/THREONINE PROTEIN PHOSPHATASE PP1 SMOOTH MUSCLE REGULATORY M110 SUBUNIT (110 KDA SUBUNIT) - RATTUS NORVEGICUS (RAT), 976 aa.	0.00E+00	12

348	cg43920534	4785	CATGAAGAGGTG TCCAGCCATCAT A[A/G]TCTTTAAT ATTAACATCATA GCCTG	A	G	Asp	Asp	SILENT-CODING	phosphatase	Human Gene SPTREMBL-ID:Q10728 SERINE/THREONINE PROTEIN PHOSPHATASE PP1 SMOOTH MUSCLE REGULATORY M110 SUBUNIT (110 KDA SUBUNIT) - RATTUS NORVEGICUS (RAT), 976 aa.	0.00E+00	12
349	cg43920534	4836	CCTGTATTAAAA GTTTTAAAACTTC [T/C]GTATACCCT TTGGCCGCTGCC ACGT	T	C	Thr	Thr	SILENT-CODING	phosphatase	Human Gene SPTREMBL-ID:Q10728 SERINE/THREONINE PROTEIN PHOSPHATASE PP1 SMOOTH MUSCLE REGULATORY M110 SUBUNIT (110 KDA SUBUNIT) - RATTUS NORVEGICUS (RAT), 976 aa.	0.00E+00	12
350	cg43920534	4842	TTAAAAGTTTTAA AACTTCTGTATA[C/G]CCTTTGGCC GCTGCCACGTG GAGTG	C	G	Gly	Gly	SILENT-CODING	phosphatase	Human Gene SPTREMBL-ID:Q10728 SERINE/THREONINE PROTEIN PHOSPHATASE *PP1* SMOOTH MUSCLE REGULATORY M110 SUBUNIT (110 KDA SUBUNIT) - RATTUS NORVEGICUS (RAT), 976 aa.	0.00E+00	12
351	cg43920534	4851	TTAAAACTTCTGT ATACCCTTTGGC[C/A]GCTGCCACG TGGAGTGCTGTG CCTC	C	A	Ala	Ala	SILENT-CODING	phosphatase	Human Gene SPTREMBL-ID:Q10728 SERINE/THREONINE PROTEIN PHOSPHATASE PP1 SMOOTH MUSCLE REGULATORY M110 SUBUNIT (110 KDA SUBUNIT) - RATTUS NORVEGICUS (RAT), 976 aa.	0.00E+00	12
352	cg43920534	4857	CTTCTGTATACC CTTTGGCCGCTG C[C/A]ACGTGGA GTGCTGTGCCTC CGGATT	C	A	Val	Val	SILENT-CODING	phosphatase	Human Gene SPTREMBL-ID:Q10728 SERINE/THREONINE PROTEIN PHOSPHATASE PP1 SMOOTH MUSCLE REGULATORY M110 SUBUNIT (110 KDA SUBUNIT) - RATTUS NORVEGICUS (RAT), 976 aa.	0.00E+00	12
353	cg43920534	4863	TATACCCTTTGG CCGCTGCCACGT G[G/A]AGTGCTG TGCCTCCGGATT TTGCAT	G	A	Leu	Leu	SILENT-CODING	phosphatase	Human Gene SPTREMBL-ID:Q10728 SERINE/THREONINE PROTEIN PHOSPHATASE PP1 SMOOTH MUSCLE REGULATORY M110 SUBUNIT (110 KDA SUBUNIT) - RATTUS NORVEGICUS (RAT), 976 aa.	0.00E+00	12

354	cg43920534	4872	TGGCCGCTGCC ACGTGGAGTGCT GT[G/A]CCTCCG GATTTTGCATGC CGGACAT	G	A	Gly	Gly	SILENT-CODING	phosphatase	Human Gene SPTREMBL-ID:Q10728 SERINE/THREONINE PROTEIN PHOSPHATASE PP1 SMOOTH MUSCLE REGULATORY M110 SUBUNIT (110 KDA SUBUNIT) - RATTUS NORVEGICUS (RAT), 976 aa.	0.00E+00	12
355	cg43920534	4878	CTGCCACGTGGA GTGCTGTGCCTC C[G/A]GATTTTGC ATGCCGGACATC ATTTA	G	A	Ser	Ser	SILENT-CODING	phosphatase	Human Gene SPTREMBL-ID:Q10728 SERINE/THREONINE PROTEIN PHOSPHATASE PP1 SMOOTH MUSCLE REGULATORY M110 SUBUNIT (110 KDA SUBUNIT) - RATTUS NORVEGICUS (RAT), 976 aa.	0.00E+00	12
356	cg43321833	2271	CTAACACTGTGG AACCAGAGAAGC A[A/G]GGGGAGA ACACCATGAAGA TGACTG	A	G	Gln	Gln	SILENT-CODING	phosphatase	Human Gene TREMBLNEW-ID:G2828708 RECEPTOR PROTEIN TYROSINE PHOSPHATASE - HOMO SAPIENS (HUMAN), 1461 aa (fragment).	0.00E+00	20
357	cg43326090	1070	CATCATCTACAT TGGAGAGCTTCA C[A/T]CGCGTGG CATCATAGGGCA ATATAT	A	T	Arg	Arg	SILENT-CODING	phosphatase	Human Gene SWISSPROT-ID:P23467 PROTEIN-TYROSINE PHOSPHATASE BETA PRECURSOR (EC 3.1.3.48) (R-PTP- BETA) - HOMO SAPIENS (HUMAN), 1997 aa.	0.00E+00	12 (12q15)
358	cg42548845	1611	TGAAAAAGCTCA TCGAAGAGAAGG A[C/T]TTTCAAAT GCTGTATGCATA TGATC	C	T	Asp	Asp	SILENT-CODING	phosphatase	Human Gene SWISSPROT-ID:P32019 TYPE II INOSITOL-1,4,5-TRISPHOSPHATE 5-PHOSPHATASE PRECURSOR (EC 3.1.3.56) (5PTASE) - HOMO SAPIENS (HUMAN), 942 aa (fragment).	0.00E+00	
359	cg43918944	997	TCCGGACACTTC CTCCAAGTGATA A[C/T]CCAGACTT TGACCCGGAAGA GGATG	C	T	Asn	Asn	SILENT-CODING	phosphatase	Human Gene SPTREMBL-ID:Q15172 PROTEIN PHOSPHATASE 2A B56-ALPHA - HOMO SAPIENS (HUMAN), 486 aa.	4.60E-246	1
360	cg43918944	1003	CACTTCCTCCAA GTGATAACCCAG A[C/T]TTTGACCC GGAAGAGGATG AGCCCA	C	T	Asp	Asp	SILENT-CODING	phosphatase	Human Gene SPTREMBL-ID:Q15172 PROTEIN PHOSPHATASE 2A B56-ALPHA - HOMO SAPIENS (HUMAN), 486 aa.	4.60E-246	1

361	cg43918944	1009	CTCCAAGTGATAACCCAGACTTTGA[C/T]CCGGAAGAGGATGAGCCCACACTTG	C	T	Asp	Asp	SILENT-CODING	phosphatase	Human Gene SPTREMBL-ID:Q15172 PROTEIN PHOSPHATASE 2A B56-ALPHA - HOMO SAPIENS (HUMAN), 486 aa.	4.60E-246	1
362	cg43918944	1012	CAAGTGATAACCCAGACTTTGACCC[G/A]GAAGAGGATGAGCCCACACTTGAGG	G	A	Pro	Pro	SILENT-CODING	phosphatase	Human Gene SPTREMBL-ID:Q15172 PROTEIN PHOSPHATASE 2A B56-ALPHA - HOMO SAPIENS (HUMAN), 486 aa.	4.60E-246	1
363	cg43918944	1024	CAGACTTTGACCCGGAAGAGGATGA[G/A]CCCACACTTGAGGCCTCTTGGCCTC	G	A	Glu	Glu	SILENT-CODING	phosphatase	Human Gene SPTREMBL-ID:Q15172 PROTEIN PHOSPHATASE 2A B56-ALPHA - HOMO SAPIENS (HUMAN), 486 aa.	4.60E-246	1
364	cg43918944	1030	TTGACCCGGAAGAGGATGAGCCCAC[A/G]CTTGAGGCCTCTTGGCCTCACATAC	A	G	Thr	Thr	SILENT-CODING	phosphatase	Human Gene SPTREMBL-ID:Q15172 PROTEIN PHOSPHATASE 2A B56-ALPHA - HOMO SAPIENS (HUMAN), 486 aa.	4.60E-246	1
365	cg43918944	1084	TGGTGTATGAATTCTTCTTGAGATT[C/T]TTGGAGAGTCCTGATTTCCAGCCCA	C	T	Phe	Phe	SILENT-CODING	phosphatase	Human Gene SPTREMBL-ID:Q15172 PROTEIN PHOSPHATASE 2A B56-ALPHA - HOMO SAPIENS (HUMAN), 486 aa.	4.60E-246	1
366	cg43918944	1108	TCTTGGAGAGTCCTGATTTCCAGCC[C/T]AGCATTGCAAAGCGATACATTGACC	C	T	Pro	Pro	SILENT-CODING	phosphatase	Human Gene SPTREMBL-ID:Q15172 PROTEIN PHOSPHATASE 2A B56-ALPHA - HOMO SAPIENS (HUMAN), 486 aa.	4.60E-246	1
367	cg43918944	976	AAATGATCAGTGCTAACATCTTCCG[G/T]ACACTTCCTCCAAGTGATAACCCAG	G	T	Arg	Arg	SILENT-CODING	phosphatase	Human Gene SPTREMBL-ID:Q15172 PROTEIN PHOSPHATASE 2A B56-ALPHA - HOMO SAPIENS (HUMAN), 486 aa.	4.60E-246	1

368	cg43988504	819	CTTCTGTCTGGC TGATACCTGCCT C[T/C]TGCTGATG GACAAGAGGAAA GACCC	T	C	Leu	Leu	SILENT-CODING	phosphatase	Human Gene SWISSNEW-ID:P18031 PROTEIN-TYROSINE PHOSPHATASE 1B (EC 3.1.3.48) (PTP-1B) - HOMO SAPIENS (HUMAN), 435 aa.\|pcls:SWISSPROT-ID:P18031 PROTEIN-TYROSINE PHOSPHATASE 1B (EC 3.1.3.48) (PTP-1B) - HOMO SAPIENS (HUMAN), 435 aa.	8.00E-242	20 (20q13.1)
369	cg43988504	900	AGAAATGAGGAA GTTTCGGATGGG G[C/T]TGATCCAG ACAGCCGACCA GCTGCG	C	T	Leu	Leu	SILENT-CODING	phosphatase	Human Gene SWISSNEW-ID:P18031 PROTEIN-TYROSINE PHOSPHATASE 1B (EC 3.1.3.48) (PTP-1B) - HOMO SAPIENS (HUMAN), 435 aa.\|pcls:SWISSPROT-ID:P18031 PROTEIN-TYROSINE PHOSPHATASE 1B (EC 3.1.3.48) (PTP-1B) - HOMO SAPIENS (HUMAN), 435 aa.	8.00E-242	20 (20q13.1)
370	cg43933809	4446	CAAATAATCTCA GTAAATCTGTAT A[T/C]TGTCCATG AATATCTCCACA AATTT	T	C	Gln	Gln	SILENT-CODING	phosphatase	Human Gene SWISSPROT-ID:P37140 SERINE/THREONINE PROTEIN PHOSPHATASE PP1-BETA CATALYTIC SUBUNIT (EC 3.1.3.16) (PP-1B) - HOMO SAPIENS (HUMAN), RATTUS NORVEGICUS (RAT), MUS MUSCULUS (MOUSE),, 327 aa.	1.60E-181	2 (2p23)
371	cg43269274	1510	CAGCCTCACAGT GGACCAGGACC TT[G/T]CCTCCCT TTTCCCTGACAC AGTCAA	G	T	Gly	Gly	SILENT-CODING	phosphatase	Human Gene SWISSPROT-ID:Q16690 DUAL SPECIFICITY PROTEIN PHOSPHATASE 5 (EC 3.1.3.48) (EC 3.1.3.16) (DUAL SPECIFICITY PROTEIN PHOSPHATASE HVH3) - HOMO SAPIENS (HUMAN), 384 aa.	3.20E-151	10
372	cg43269274	1674	ACATTCAGCAGG GCTGTGATGTGC A[A/G]GTTGGCG AGGAACTCGCAC TTGGAT	A	G	Leu	Leu	SILENT-CODING	phosphatase	Human Gene SWISSPROT-ID:Q16690 DUAL SPECIFICITY PROTEIN PHOSPHATASE 5 (EC 3.1.3.48) (EC 3.1.3.16) (DUAL SPECIFICITY PROTEIN PHOSPHATASE HVH3) - HOMO SAPIENS (HUMAN), 384 aa.	3.20E-151	10

373	cg44021995	2412	TTTTAAGTAAAGTAGTGGACAGCCT[G/A]GCCCCATCCATTACTAATGTTTTAG	G	A	Leu	Leu	SILENT-CODING	phosphorylase	Human Gene SWISSNEW-ID:Q93100 PHOSPHORYLASE B KINASE BETA REGULATORY CHAIN (PHOSPHORYLASE KINASE BETA SUBUNIT) - HOMO SAPIENS (HUMAN), 1092 aa.\|pcls:SWISSPROT-ID:Q93100 PHOSPHORYLASE B KINASE BETA REGULATORY CHAIN (PHOSPHORYLASE KINASE BETA SUBUNIT) - HOMO SAPIENS (HUMAN), 1092 aa.	0.00E+00	16
374	cg42688448	1787	GAGGAGCACCTGTGGGGGTTGCAGG[A/G]CGAGGCGCCATGGTAGTCTGAGGCT	A	G	Arg	Arg	SILENT-CODING	polymerase	Human Gene SPTREMBL-ID:O00268 SUBUNIT OF RNA POLYMERASE II TRANSCRIPTION FACTOR TFIID - HOMO SAPIENS (HUMAN), 1083 aa.	0.00E+00	20
375	cg42688448	1790	GAGCACCTGTGGGGGTTGCAGGACG[A/G]GGCGCCATGGTAGTCTGAGGCTGGG	A	G	Pro	Pro	SILENT-CODING	polymerase	Human Gene SPTREMBL-ID:O00268 SUBUNIT OF RNA POLYMERASE II TRANSCRIPTION FACTOR TFIID - HOMO SAPIENS (HUMAN), 1083 aa.	0.00E+00	20
376	cg42688448	1793	CACCTGTGGGGGTTGCAGGACGAGG[C/T]GCCATGGTAGTCTGAGGCTGGGCAT	C	T	Ala	Ala	SILENT-CODING	polymerase	Human Gene SPTREMBL-ID:O00268 SUBUNIT OF RNA POLYMERASE II TRANSCRIPTION FACTOR TFIID - HOMO SAPIENS (HUMAN), 1083 aa.	0.00E+00	20
377	cg42688448	1826	TAGTCTGAGGCTGGGCATGGGCATG[G/C]GCCTGCATCTGGGCCAAGGCCTGCT	G	C	Ala	Ala	SILENT-CODING	polymerase	Human Gene SPTREMBL-ID:O00268 SUBUNIT OF RNA POLYMERASE II TRANSCRIPTION FACTOR TFIID - HOMO SAPIENS (HUMAN), 1083 aa.	0.00E+00	20
378	cg42688448	1856	GCATCTGGGCCAAGGCCTGCTGAGG[A/G]ATCATTAACAACTGCCCATTCTCAC	A	G	Ile	Ile	SILENT-CODING	polymerase	Human Gene SPTREMBL-ID:O00268 SUBUNIT OF RNA POLYMERASE II TRANSCRIPTION FACTOR TFIID - HOMO SAPIENS (HUMAN), 1083 aa.	0.00E+00	20

379	cg42688448	1940	AGTTCTGGATGTTGGTCGGGTTCTG[A/C]GGCGGCTGCGGCAAGCGCGGGGCCA	A	C	Pro	Pro	SILENT-CODING	polymerase	Human Gene SPTREMBL-ID:O00268 SUBUNIT OF RNA POLYMERASE II TRANSCRIPTION FACTOR TFIID - HOMO SAPIENS (HUMAN), 1083 aa.	0.00E+00	20
380	cg42688448	1954	GTCGGGTTCTGAGGCGGCTGCGGCA[A/G]GCGCGGGGCCAGCACGGTGGGCGTC	A	G	Leu	Leu	SILENT-CODING	polymerase	Human Gene SPTREMBL-ID:O00268 SUBUNIT OF RNA POLYMERASE II TRANSCRIPTION FACTOR TFIID - HOMO SAPIENS (HUMAN), 1083 aa.	0.00E+00	20
381	cg43968623	801	TCTTGGAAGATGAACTGCAGCGTAT[A/C]AAACTAAAAGGCACCATTGAAGTGT	A	C	Ile	Ile	SILENT-CODING	polymerase	Human Gene SWISSNEW-ID:P49004 DNA POLYMERASE DELTA SMALL SUBUNIT (EC 2.7.7.7) - BOS TAURUS (BOVINE), 469 aa.\|pcls:SWISSPROT-ID:P49004 DNA POLYMERASE DELTA SMALL SUBUNIT (EC 2.7.7.7) - BOS TAURUS (BOVINE), 469 aa.	7.00E-199	
382	cg43311989	248	ACTTCGAATAAAGTTGTTCCAATGA[G/A]GACTGCATAGTTTCCAAATAACCAG	G	A	Ser	Ser	SILENT-CODING	polymerase	Human Gene SPTREMBL-ID:O00419 MITOCHONDRIAL DNA POLYMERASE ACCESSORY SUBUNIT PRECURSOR - HOMO SAPIENS (HUMAN), 372 aa.	1.90E-197	
383	cg43993893	502	ACTCATTGATTGTGAAACCCTTTTC[T/C]AGGGCATGAGCCCTCATATTCTTAT	T	C	Leu	Leu	SILENT-CODING	polymerase	Human Gene SWISSNEW-ID:P06746 DNA POLYMERASE BETA (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 334 aa.\|pcls:SWISSPROT-ID:P06746 DNA POLYMERASE BETA (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 334 aa.	5.00E-178	8 (8p11.2)
384	cg43993893	679	CCATGAACTTTGTCTCACCCTTTGA[C/A]AGGGTATCTGTGATAAAATGAACCT	C	A	Leu	Leu	SILENT-CODING	polymerase	Human Gene SWISSNEW-ID:P06746 DNA POLYMERASE BETA (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 334 aa.\|pcls:SWISSPROT-ID:P06746 DNA POLYMERASE BETA (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 334 aa.	5.00E-178	8 (8p11.2)

385	cg43993893	877	AATCCACTTTTTTAACTTCATTTAG[T/A]ACAATATCTTGCATTTGTAACATCT	T	A	Val	Val	SILENT-CODING	polymerase	Human Gene SWISSNEW-ID:P06746 DNA POLYMERASE BETA (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 334 aa.\|pcls:SWISSPROT-ID:P06746 DNA POLYMERASE BETA (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 334 aa.	5.00E-178	8 (8p11.2)
386	cg43916712	4150	TGTGAGCAATGAATTCATCATGAAG[G/A]ACTGAGGAATTGGCATCAATCTGAA	G	A	Val	Val	SILENT-CODING	polymerase	Human Gene Homologous to SWISSNEW-ID:P19387 DNA-DIRECTED RNA POLYMERASE II 33 KD POLYPEPTIDE (EC 2.7.7.6) (RPB3) (RPB33) (RPB31) - HOMO SAPIENS (HUMAN), 275 aa.	6.20E-148	
387	cg42876552	418	CTTTCTGCAAATCAATAGGCACAGA[T/G]ATGCGACCTGTTTTAGGATGAACAC	T	G	Ile	Ile	SILENT-CODING	polymerase	Human Gene Similar to SWISSPROT-ID:Q24317 DNA PRIMASE SMALL SUBUNIT (EC 2.7.7.-) (DNA PRIMASE 50 KD SUBUNIT) (DNA POLYMERASE SUBUNIT A) (DPRI50) - DROSOPHILA MELANOGASTER (FRUIT FLY), 438 aa.	2.20E-88	12 (12q13)
388	cg43948227	366	TCGAATTTTACAGTTTTCTTACTGC[A/G]TCATCAATGTCAGAAATCTGTTCCT	A	G	Asp	Asp	SILENT-CODING	polymerase	Human Gene Similar to SWISSNEW-ID:P53999 ACTIVATED RNA POLYMERASE II TRANSCRIPTIONAL COACTIVATOR P15 (PC4) (P14) - HOMO SAPIENS (HUMAN), 126 aa.\|pcls:SWISSPROT-ID:P53999 ACTIVATED RNA POLYMERASE II TRANSCRIPTIONAL COACTIVATOR P15 (PC4) (P14) - HOMO SAPIENS (HUMAN), 126 aa.	5.40E-62	5
389	cg42534568	612	AGCGCGTCCACATCAACATCTCCGG[G/C]CTGCGCTTTGAGACGCAGCTGGGCA	G	C	Gly	Gly	SILENT-CODING	potassium_channel	Human Gene SWISSPROT-ID:P22460 VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.5 (HK2) (HPCN1) - HOMO SAPIENS (HUMAN), 613 aa.	0.00E+00	12 (12p13)

390	cg42937321	1388	ATATGCACCCAG TGACCATAGGGG G[C/G]AAGATTGT GGGATCTCTCTG TGCCA	C	G	Gly	Gly	SILENT-CODING	potassium_channel	Human Gene SWISSPROT-ID:P22001 VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.3 (HPCN3) (HGK5) (HUKIII) (HLK3) - HOMO SAPIENS (HUMAN), 523 aa.	5.40E-284	1 (1p21)
391	cg42937321	353	AGCGCGTGGTC ATCAACATCTCC GG[G/C]CTGCGC TTCGAGACGCAG CTGAAGA	G	C	Gly	Gly	SILENT-CODING	potassium_channel	Human Gene SWISSPROT-ID:P22001 VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.3 (HPCN3) (HGK5) (HUKIII) (HLK3) - HOMO SAPIENS (HUMAN), 523 aa.	5.40E-284	1 (1p21)
392	cg43331104	878	CCTTCTTCATCG TGGAAACGCTGT G[T/C]ATCATCTG GTTCTCCTTCGA GCTGG	T	C	Cys	Cys	SILENT-CODING	potassium_channel	Human Gene SWISSPROT-ID:Q09470 VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.1 (HUKI) (HBK1) - HOMO SAPIENS (HUMAN), 495 aa.	5.60E-266	12
393	cg43992375	3210	GATTCACTGGAT TTTGGCAGACCC A[A/G]CTTGGGG CTCGGGATGTCT GCACAG	A	G	Leu	Leu	SILENT-CODING	potassium_channel	Human Gene SPTREMBL-ID:Q16547 POTASSIUM CHANNEL BETA3 SUBUNIT - HOMO SAPIENS (HUMAN), 408 aa.	1.30E-218	3
394	cg43951366	505	TTCGAAATGCAA TTATGAGTTATG T[G/C]TTGACATC CAGATCACATTT GATTG	G	C	Val	Val	SILENT-CODING	prostaglandin	Human Gene SWISSNEW-ID:P35354 PROSTAGLANDIN G/H SYNTHASE 2 PRECURSOR (EC 1.14.99.1) (CYCLOOXYGENASE -2) (COX-2) (PROSTAGLANDIN-ENDOPEROXIDE SYNTHASE 2) (PROSTAGLANDIN H2 SYNTHASE 2) (PGH SYNTHASE 2) (PGHS-2) (PHS II) - HOMO SAPIENS (HUMAN), 604 aa.\|pcls:SPTREMBL-ID:Q16876 PROSTAGLANDIN ENDOPEROXIDE SYNTHASE-2 PRECURSOR (EC 1.14.99.1) (PROSTAGLANDIN-ENDOPEROXIDE SYNTHASE) (PROSTAGLANDIN SYNTHASE) (PROSTAGLANDIN G/H SYNTHASE) - HOMO SAPIENS (HUMAN), 604 aa.	0.00E+00	1 (1q25.2)

395	cg43986296	1743	ACTCATCCCCGACATCCCTGATGAC[A/C]AGCCTGTAGGTCCCTCGGGCTCTCT	A	C	Leu	Leu	SILENT-CODING	protease	Human Gene SPTREMBL-ID:Q62849 SERINE PROTEINASE RPC7 PRECURSOR - RATTUS NORVEGICUS (RAT), 783 aa.	4.60E-223	
396	cg43982119	1306	GCTTGGTTTTTTTCTTTTTGACTGG[T/C]CGATCCACGCAGATGGTATTTTCAA	T	C	Arg	Arg	SILENT-CODING	protease	Human Gene SWISSPROT-ID:P20807 CALPAIN P94, LARGE (CATALYTIC) SUBUNIT (EC 3.4.22.17) (CALCIUM-ACTIVATED NEUTRAL PROTEINASE) (CANP) (P94 PROTEIN) (MUSCLE-SPECIFIC CALCIUM-ACTIVATED NEUTRAL PROTEASE 3 LARGE SUBUNIT) - HOMO SAPIENS (HUMAN), 821 aa.	5.70E-161	15
397	cg43306871	1105	GCTCGCCCTGAAGAAGCAGCAGGTG[G/A]TCATCCCCTACTCGAGCCCACAGTG	G	A	Asp	Asp	SILENT-CODING	protease	Human Gene SWISSNEW-ID:O43240 PROTEASE SERINE-LIKE 1 PRECURSOR (EC 3.4.21.-) (NORMAL EPITHELIAL CELL-SPECIFIC 1) - HOMO SAPIENS (HUMAN), 276 aa.\|pcls:TREMBLNEW-ID:G2558912 SERINE PROTEASE-LIKE PROTEASE - HOMO SAPIENS (HUMAN), 276 aa.	3.10E-153	19
398	cg43923853	2273	CAGACCGAGATGTCATTCCAGTGCT[T/C]TTATGAAAATTCTTATTATTAATTA	T	C	Lys	Lys	SILENT-CODING	protease	Human Gene Homologous to SWISSNEW-ID:P42574 APOPAIN PRECURSOR (EC 3.4.22.-) (CYSTEINE PROTEASE CPP32) (YAMA PROTEIN) (CPP-32) (CASPASE-3) (CASP-3) (SREBP CLEAVAGE ACTIVITY 1) (SCA-1) - HOMO SAPIENS (HUMAN), 277 aa.\|pcls:SWISSPROT-ID:P42574 APOPAIN PRECURSOR (EC 3.4.22.-) (CYSTEINE PROTEASE CPP32) (YAMA PROTEIN) (CPP-32) (CASPASE-3) (CASP-3) (SREBP CLEAVAGE ACTIVITY 1) (SCA-1) - HOMO SAPIENS (HUMAN), 277 aa.	2.00E-149	4

399	cg43074055	916	CCCTCTACGTGGACTGGATCCGTTC[C/T]ACGCTGCGCCGTGTGGAGGCCAAGG	C	T	Ser	Ser	SILENT-CODING	protease	Human Gene Homologous to SWISSPROT-ID:P24158 MYELOBLASTIN PRECURSOR (EC 3.4.21.76) (LEUKOCYTE PROTEINASE 3) (PR-3) (PR3) (AGP7) (WEGENER'S AUTOANTIGEN) (P29) (C-ANCA ANTIGEN) - HOMO SAPIENS (HUMAN), 256 aa.	5.70E-138	19 (19p13.3)
400	cg43967243	387	TCTCTGCTTCTGTAAGAATCCTGAA[T/C]TTAGGATTTTCAACTGTCACTACTC	T	C	Lys	Lys	SILENT-CODING	protease	Human Gene Homologous to SWISSNEW-ID:P34062 PROTEASOME IOTA CHAIN (EC 3.4.99.46) (MACROPAIN IOTA CHAIN) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX IOTA CHAIN) (27 KD PROSOMAL PROTEIN) (PROS-27) (P27K) - HOMO SAPIENS (HUMAN), AND RATTUS NORVEGICUS (RAT), 246 aa.\|pcls:SWISSPROT-ID:P34062 PROTEASOME IOTA CHAIN (EC 3.4.99.46) (MACROPAIN IOTA CHAIN) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX IOTA CHAIN) (27 KD PROSOMAL PROTEIN) (PROS-27) - HOMO SAPIENS (HUMAN), AND RATTUS NORVEGICUS (RAT), 246 aa.	6.40E-130	

401	cg43967243	489	ATGTAATTGCAG TTTCCACTGTCT G[T/C]TCAAATGT CCAATCAAATTT CTTCT	T	C	Glu	Glu	SILENT-CODING	protease	Human Gene Homologous to SWISSNEW-ID:P34062 PROTEASOME IOTA CHAIN (EC 3.4.99.46) (MACROPAIN IOTA CHAIN) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX IOTA CHAIN) (27 KD PROSOMAL PROTEIN) (PROS-27) (P27K) - HOMO SAPIENS (HUMAN), AND RATTUS NORVEGICUS (RAT), 246 aa.\|pcls:SWISSPROT-ID:P34062 PROTEASOME IOTA CHAIN (EC 3.4.99.46) (MACROPAIN IOTA CHAIN) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX IOTA CHAIN) (27 KD PROSOMAL PROTEIN) (PROS-27) - HOMO SAPIENS (HUMAN), AND RATTUS NORVEGICUS (RAT), 246 aa.	6.40E-130		
402	cg43930253	972	CCACATATATAA ACCATGTCGTTT C[C/T]GTGGCTG GGTGGGGCATC AGTGATG	C	T	Ser	Ser	SILENT-CODING	protease	Human Gene Homologous to SPTREMBL-ID:Q27125 CATHEPSIN B-LIKE PROTEASE - URECHIS CAUPO (INNKEEPER WORM) (SPOONWORM), 294 aa.	2.90E-102	20	
403	cg42914280	589	GCAAGCCCAGG TGTGGAGTTCCT GA[C/T]GTTGGTC ACTTCAGAACCT TTCCTG	C	T	Asp	Asp	SILENT-CODING	protease	Human Gene Similar to SWISSNEW-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa.\|pcls:SWISSPROT-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa.	2.30E-63	11 (11q23)	

404	cg43920929	1459	GATTGTCAATCATATCCCTGGTTTC[A/G]TTTTTAACCCATGCATTGATGGAAT	A	G	Asn	Asn	SILENT-CODING	proteaseinhib	Human Gene SWISSPROT-ID:P07093 GLIA DERIVED NEXIN PRECURSOR (GDN) (PROTEASE NEXIN I) (PN-1) (PROTEASE INHIBITOR 7) - HOMO SAPIENS (HUMAN), 398 aa.	1.20E-208	2
405	cg43920929	1705	TTACGCCGTATCTCATCACCATGGC[G/A]AGCTGCTTCTTGGTCCTGCCGTCCG	G	A	Leu	Leu	SILENT-CODING	proteaseinhib	Human Gene SWISSPROT-ID:P07093 GLIA DERIVED NEXIN PRECURSOR (GDN) (PROTEASE NEXIN I) (PN-1) (PROTEASE INHIBITOR 7) - HOMO SAPIENS (HUMAN), 398 aa.	1.20E-208	2
406	cg43268468	512	GCAGGGACTTGGTGACTTCGCCTTC[G/A]TAACTCAGCTTCAGCTTGGGGACAG	G	A	Tyr	Tyr	SILENT-CODING	proteaseinhib	Human Gene TREMBLNEW-ID:G299561 EPC-1=SERINE PROTEASE INHIBITOR HOMOLOG - HOMO SAPIENS, 359 aa.	2.60E-188	17 (17p13.3)
407	cg43059041	1182	TCACCATCTCTGGAGTCTATGACCT[T/C]GGAGATGTGCTGGAGGAAATGGGCA	T	C	Leu	Leu	SILENT-CODING	proteaseinhib	Human Gene Similar to SWISSPROT-ID:P17475 ALPHA-1-ANTIPROTEINASE PRECURSOR (ALPHA-1-ANTITRYPSIN) (ALPHA-1- PROTEINASE INHIBITOR) - RATTUS NORVEGICUS (RAT), 411 aa.	4.40E-83	14 (14q32.1)
408	cg43059041	1440	ACTTCACCTGGAGCAGCCTTTTCCT[G/A]GCGAGGGTTATGAACCCAGTGTAAG	G	A	Leu	Leu	SILENT-CODING	proteaseinhib	Human Gene Similar to SWISSPROT-ID:P17475 ALPHA-1-ANTIPROTEINASE PRECURSOR (ALPHA-1-ANTITRYPSIN) (ALPHA-1- PROTEINASE INHIBITOR) - RATTUS NORVEGICUS (RAT), 411 aa.	4.40E-83	14 (14q32.1)
409	cg43969711	1750	AGAGAAATTCCCTTTCTTTGGGATC[C/T]TTTATGTAAGTGTCAATAAGAAGAC	C	T	Lys	Lys	SILENT-CODING	reductase	Human Gene SWISSPROT-ID:P31350 RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE M2 CHAIN (EC 1.17.4.1) (RIBONUCLEOTIDE REDUCTASE) - HOMO SAPIENS (HUMAN), 389 aa.	1.90E-208	2 (2p25)
410	cg43969711	1984	AGTGCTGAATGTCCTTGGAGAGGTC[C/A]ACCTCCTCGGCGGTCCAAAAGGAAG	C	A	Val	Val	SILENT-CODING	reductase	Human Gene SWISSPROT-ID:P31350 RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE M2 CHAIN (EC 1.17.4.1) (RIBONUCLEOTIDE REDUCTASE) - HOMO SAPIENS (HUMAN), 389 aa.	1.90E-208	2 (2p25)

411	cg43969711	2158	GCTCCGTGGGC TCCTGGAAGATC CT[T/C]CTCGCG GTCTTGCTGGCC AGGACGC	T	C	Arg	Arg	SILENT-CODING	reductase	Human Gene SWISSPROT-ID:P31350 RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE M2 CHAIN (EC 1.17.4.1) (RIBONUCLEOTIDE REDUCTASE) - HOMO SAPIENS (HUMAN), 389 aa.	1.90E-208	2 (2p25)	
412	cg43941472	701	TCATTGAGTGTG CCGACTCTGCCC A[T/C]GGCCTGAA GGGCCACATCAT CTCTG	T	C	His	His	SILENT-CODING	reductase	Human Gene SWISSPROT-ID:P36959 GMP REDUCTASE (EC 1.6.6.8) (GUANOSINE 5'-MONOPHOSPHATE OXIDOREDUCTASE) - HOMO SAPIENS (HUMAN), 345 aa.	7.40E-184	X (Xq28)	
413	cg43987538	1820	CTGATCGCAATT TCAGGACTTCTG G[C/T]CCACCAAA TTCAAAAACTCT AACAG	C	T	Gly	Gly	SILENT-CODING	reductase	Human Gene SWISSPROT-ID:Q08257 QUINONE OXIDOREDUCTASE (EC 1.6.5.5) (NADPH:QUINONE REDUCTASE) (ZETA- CRYSTALLIN) - HOMO SAPIENS (HUMAN), 329 aa.	1.1E-171	1 (1p31)	
414	cg43286949	355	AATATCTGTTTC GTTTTAGACCAG G[C/T]CCTTTTTC TTCAATCCATGA CAGTG	C	T	Gly	Gly	SILENT-CODING	reductase	Human Gene SWISSNEW-ID:P53004 BILIVERDIN REDUCTASE A PRECURSOR (EC 1.3.1.24) (BILIVERDIN-IX ALPHA- REDUCTASE) - HOMO SAPIENS (HUMAN), 296 aa.	pcis:SWISSPROT-ID:P53004 BILIVERDIN REDUCTASE A PRECURSOR (EC 1.3.1.24) (BILIVERDIN-IX ALPHA- REDUCTASE) - HOMO SAPIENS (HUMAN), 296 aa.	1.3E-152	7
415	cg43336298	1175	CCATCTCTACAT ATAACAGAACCG G[T/C]CCACTTCC CCCAGGCCCAC CCCCAG	T	C	Gly	Gly	SILENT-CODING	reductase	Human Gene Homologous to TREMBLNEW-ID:G2947100 15-OXOPROSTAGLANDIN 13-REDUCTASE - SUS SCROFA (PIG), 329 aa.	6.70E-146		
416	cg43948290	715	TAATAGGTTTTG GCTTGTGGTTAA C[A/G]GGCATGTT GATAAACATCCA TTCAG	A	G	Thr	Thr	SILENT-CODING	reductase	Human Gene Homologous to SWISSPROT-ID:P18405 3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (EC 1.3.99.5) (STEROID 5-ALPHA-REDUCTASE 1) (SR TYPE 1) - HOMO SAPIENS (HUMAN), 259 aa.	2.90E-141	5 (5p15)	

417	cg42717608	109	CGCAGCTTAATGTGGCCTTTTCCCG[G/T]GAGCAGGCCCACAAGGTCTATGTCC	G	T	Arg	Arg	SILENT-CODING	reductase	Human Gene Similar to SWISSNEW-ID:P37040 NADPH-CYTOCHROME P450 REDUCTASE (EC 1.6.2.4) (CPR) - MUS MUSCULUS (MOUSE), 677 aa.\|pcls:SWISSPROT-ID:P37040 NADPH-CYTOCHROME P450 REDUCTASE (EC 1.6.2.4) (CPR) - MUS MUSCULUS (MOUSE), 677 aa.	1.80E-51	
418	cg43257152	622	CTACCAAGACTTTGAGAATCACTAC[A/G]AGAAAAACTCCTTGTGGTGAAGGTT	A	G	Thr	Thr	SILENT-CODING	ribosomal prot	Human Gene Similar to SWISSPROT-ID:P17075 40S RIBOSOMAL PROTEIN S20 - HOMO SAPIENS (HUMAN), AND RATTUS NORVEGICUS (RAT), 119 aa.	8.2E-59	3
419	cg44937448	365	TCCTGTTCACCAACCGCACAAAGGA[G/A]GAGGTGAATGAGTGGTTCACGAAAT	G	A	Glu	Glu	SILENT-CODING	ribosomal prot	Human Gene Similar to SPTREMBL-ID:Q19302 SIMILAR TO 60S ACIDIC RIBOSOMAL PROTEIN PO - CAENORHABDITIS ELEGANS, 220 aa.	5.3E-55	7
420	cg43255045	5515	GCGAGGAGGAACAGCTACGCCAGGA[A/G]AGGGAAGAACAGCAGCTGCGCCCCC	A	G	Glu	Glu	SILENT-CODING	struct	Human Gene SWISSPROT-ID:Q07283 TRICHOHYALIN - HOMO SAPIENS (HUMAN), 1898 aa.	0	1
421	cg43927378	843	TCCTGGGTGCTGGCCCTGTGCTGGA[G/A]GCTTTTGGAAATGCCAAGACAGCCC	G	A	Glu	Glu	SILENT-CODING	struct	Human Gene SPTREMBL-ID:Q13459 MYOSIN-IXB - HOMO SAPIENS (HUMAN), 2022 aa.	0	2
422	cg44033566	3341	AGGCCTGGCTCTCCATCACCCAGAA[A/G]GCTGTGGCCTCTGAGGACATGCCCG	A	G	Lys	Lys	SILENT-CODING	struct	Human Gene SWISSNEW-ID:P11277 SPECTRIN BETA CHAIN, ERYTHROCYTE - HOMO SAPIENS (HUMAN), 2137 aa.\|pcls:SWISSPROT-ID:P11277 SPECTRIN BETA CHAIN, ERYTHROCYTE - HOMO SAPIENS (HUMAN), 2137 aa.	0	14 (14q22)

423	cg43131005	8940	ACAGATATCTCT TTAAGGAAGTTG C[A/G]GGGCCAA CAGAAATGTGTG ACCAGA	A	G	Ala	Ala	SILENT-CODING	struct	Human Gene SWISSPROT-ID:P46939 UTROPHIN (DYSTROPHIN-RELATED PROTEIN 1) (DRP1) (DRP) - HOMO SAPIENS (HUMAN), 3433 aa.	0	
424	cg43131005	8946	ATCTCTTTAAGG AAGTTGCAGGGC C[A/G]ACAGAAAT GTGTGACCAGAG GCAGC	A	G	Pro	Pro	SILENT-CODING	struct	Human Gene SWISSPROT-ID:P46939 UTROPHIN (DYSTROPHIN-RELATED PROTEIN 1) (DRP1) (DRP) - HOMO SAPIENS (HUMAN), 3433 aa.	0	
425	cg43249606	108	ACACACCTGGAA GCCATTGAGAGC A[G/A]CTGGAGAT GGAGTGGCAGC TGGAGT	G	A	Ser	Ser	SILENT-CODING	struct	Human Gene SWISSNEW-ID:Q01082 SPECTRIN BETA CHAIN, BRAIN (SPECTRIN, NON-ERYTHROID BETA CHAIN) (FODRIN BETA CHAIN) (SPTBN1) - HOMO SAPIENS (HUMAN), 2364 aa.\|pcls:SWISSPROT-ID:Q01082 SPECTRIN BETA CHAIN, BRAIN (SPECTRIN, NON-ERYTHROID BETA CHAIN) (FODRIN BETA CHAIN) (SPTBN1) - HOMO SAPIENS (HUMAN), 2364 aa.	0	
426	cg44918439	1208	AAAAGGAAAAGG AAAGAATAGAAC G[C/T]GTGAAGG AAGAGCTAATGG AACGTC	C	T	Arg	Arg	SILENT-CODING	struct	Human Gene SWISSPROT-ID:P35241 RADIXIN - HOMO SAPIENS (HUMAN), 583 aa.	9.3e-312	11 (11q23)
427	cg44918439	1508	CCAAGAAGAAAA AGGAAGAGGAA GC[T/A]ACTGAGT GGCAACACAAAG CTTTTG	T	A	Ala	Ala	SILENT-CODING	struct	Human Gene SWISSPROT-ID:P35241 RADIXIN - HOMO SAPIENS (HUMAN), 583 aa.	9.3e-312	11 (11q23)
428	cg43980812	870	GAAGCTGGGCC CGGCATGTAGAA CA[C/T]ACAAAGC AGCCCACGTGAA AGACGC	C	T	Val	Val	SILENT-CODING	struct	Human Gene SWISSNEW-ID:Q15654 THYROID RECEPTOR INTERACTING PROTEIN 6 (TRIP6) (OPA-INTERACTING PROTEIN 1) (ZYXIN RELATED PROTEIN 1) (ZRP-1) - HOMO SAPIENS (HUMAN), 476 aa.	2.9E-272	7

429	cg43987609	1752	CAGTTCTTTTCA AATCTCTTTGCA A[G/A]CGACGTC CAAAGTCCCTGA ACATGG	G	A	Arg	Arg	SILENT-CODING	struct	Human Gene SWISSPROT-ID:P32391 ACTIN-LIKE PROTEIN 3 (ACTIN-2) - HOMO SAPIENS (HUMAN), AND BOS TAURUS (BOVINE), 418 aa.	1.1E-226	2
430	cg43987609	1785	CAAAGTCCCTGA ACATGGTTGAAC C[T/A]CCAGAGA GGACAATATTCT TGTAGA	T	A	Gly	Gly	SILENT-CODING	struct	Human Gene SWISSPROT-ID:P32391 ACTIN-LIKE PROTEIN 3 (ACTIN-2) - HOMO SAPIENS (HUMAN), AND BOS TAURUS (BOVINE), 418 aa.	1.1E-226	2
431	cg11751474	312	ACGACACCCATC AGCACCACCACC A[C/T]GGTGACC CCAACCCCAACA CCCACT	C	T	His	His	SILENT-CODING	struct	Human Gene SPTREMBL-ID:Q99322 MUCIN CORE POLYPEPTIDE, TRACHEAL - HOMO SAPIENS (HUMAN), 295 aa (fragment).	3.6E-189	
432	cg43916919	421	CAGATATCAGCA GTTCAAGGGCAA A[T/G]GGGCTGG AGTCAGCCACCT TGGTCA	T	G	Pro	Pro	SILENT-CODING	struct	Human Gene SWISSNEW-ID:P40121 MACROPHAGE CAPPING PROTEIN (ACTIN-REGULATORY PROTEIN CAP-G) - HOMO SAPIENS (HUMAN), 348 aa.\|pcls:SWISSPROT-ID:P40121 MACROPHAGE CAPPING PROTEIN (ACTIN-REGULATORY PROTEIN CAP-G) - HOMO SAPIENS (HUMAN), 348 aa.	4.30E-188	2 (2cen)
433	cg43304066	2468	TTTGCTTCCGAG CTTCTTCCCCCG C[G/A]GAGCTGA GGTTCCTTAGGC AACCTG	G	A	Ser	Ser	SILENT-CODING	struct	Human Gene SPTREMBL-ID:O00379 DELTA-CATENIN - HOMO SAPIENS (HUMAN), 792 aa.	2.20E-186	2
434	cg43304066	2495	AGCTGAGGTTCC TTAGGCAACCTG T[C/T]GTGTTACG CAGAACTAGTGA AGTCT	C	T	Thr	Thr	SILENT-CODING	struct	Human Gene SPTREMBL-ID:O00379 DELTA-CATENIN - HOMO SAPIENS (HUMAN), 792 aa.	2.20E-186	2
435	cg43949677	478	TCATGAGTAACC AGCAGTACTACC A[A/G]GCCCTGA GCAGCAGCTCCA TCATGA	A	G	Gln	Gln	SILENT-CODING	struct	Human Gene SWISSPROT-ID:P28289 TROPOMODULIN - HOMO SAPIENS (HUMAN), 359 aa.	2.40E-185	9 (9q22.2)

436	cg43949677	802	TCAAGGAGAACA AGGTGTTGAAGA C[C/A]CTGAATGT GGAATCCAACTT CATTT	C	A	Thr	Thr	SILENT-CODING	struct	Human Gene SWISSPROT-ID:P28289 TROPOMODULIN - HOMO SAPIENS (HUMAN), 359 aa.	2.40E-185	9 (9q22.2)
437	cg43949677	865	TTCTGCGCCTGG TAGAAGCCCTCC C[C/A]CACAACAC TTCTCTGGTCGA GCTGA	C	A	Pro	Pro	SILENT-CODING	struct	Human Gene SWISSPROT-ID:P28289 TROPOMODULIN - HOMO SAPIENS (HUMAN), 359 aa.	2.40E-185	9 (9q22.2)
438	cg43962437	1215	ACGGCGATGCA GGCTACGGGCA GGG[G/C]CCCGG CGGGTACGGGC CCCAGGATT	G	C	Gly	Gly	SILENT-CODING	struct	Human Gene SWISSNEW-ID:P08247 SYNAPTOPHYSIN (MAJOR SYNAPTIC VESICLE PROTEIN P38) - HOMO SAPIENS (HUMAN), 313 aa.\|pcls:SWISSPROT-ID:P08247 SYNAPTOPHYSIN (MAJOR SYNAPTIC VESICLE PROTEIN P38) - HOMO SAPIENS (HUMAN), 313 aa.\|pcls:TREMBLNEW-ID:G2707601 SYNAPTOPHYSIN - HOMO SAPIENS (HUMAN), 313 aa.	4.80E-173	X (Xp11.23)
439	cg43956325	1173	CCTTAACAATCA GCTGCCGCTGT GC[A/G]TTTGACC TCTCAGTCAGAA TGCTGA	A	G	Asn	Asn	SILENT-CODING	struct	Human Gene SWISSPROT-ID:P12429 ANNEXIN III (LIPOCORTIN III) (PLACENTAL ANTICOAGULANT PROTEIN III) (PAP-III) (35-ALPHA CALCIMEDIN) (INOSITOL 1,2-CYCLIC PHOSPHATE 2-PHOSPHOHYDROLASE) - HOMO SAPIENS (HUMAN), 323 aa.	3.10E-169	4 (4q21)
440	cg43956325	1181	ATCAGCTGCCGC TGTGCATTTGAC C[T/G]CTCAGTCA GAATGCTGATGA GCATT	T	G	Arg	Arg	SILENT-CODING	struct	Human Gene SWISSPROT-ID:P12429 ANNEXIN III (LIPOCORTIN III) (PLACENTAL ANTICOAGULANT PROTEIN III) (PAP-III) (35-ALPHA CALCIMEDIN) (INOSITOL 1,2-CYCLIC PHOSPHATE 2-PHOSPHOHYDROLASE) - HOMO SAPIENS (HUMAN), 323 aa.	3.10E-169	4 (4q21)

441	cg43956325	1185	GCTGCCGCTGTGCATTTGACCTCTC[A/C]GTCAGAATGCTGATGAGCATTTTCT	A	C	Thr	Thr	SILENT-CODING	struct	Human Gene SWISSPROT-ID:P12429 ANNEXIN III (LIPOCORTIN III) (PLACENTAL ANTICOAGULANT PROTEIN III) (PAP-III) (35-ALPHA CALCIMEDIN) (INOSITOL 1,2-CYCLIC PHOSPHATE 2-PHOSPHOHYDROLASE) - HOMO SAPIENS (HUMAN), 323 aa.	3.10E-169	4 (4q21)
442	cg43956325	1212	TCAGAATGCTGATGAGCATTTTCTC[A/G]TCAGTTCCAATTCCTCTGATTGCTT	A	G	Asp	Asp	SILENT-CODING	struct	Human Gene SWISSPROT-ID:P12429 ANNEXIN III (LIPOCORTIN III) (PLACENTAL ANTICOAGULANT PROTEIN III) (PAP-III) (35-ALPHA CALCIMEDIN) (INOSITOL 1,2-CYCLIC PHOSPHATE 2-PHOSPHOHYDROLASE) - HOMO SAPIENS (HUMAN), 323 aa.	3.10E-169	4 (4q21)
443	cg43985529	889	GCTCCATGGCCGTCTGCAAGGGCGC[C/G]GGCTCCTGGGCTGGGCTTACGAGAC	C	G	Pro	Pro	SILENT-CODING	struct	Human Gene SPTREMBL-ID:Q95264 CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE II ISOFORM GAMMA-E - SUS SCROFA (PIG), 334 aa (fragment).	1.00E-163	
444	cg43985529	895	TGGCCGTCTGCAAGGGCGCCGGCTC[C/T]TGGGCTGGGCTTACGAGACTGTTTT	C	T	Gln	Gln	SILENT-CODING	struct	Human Gene SPTREMBL-ID:Q95264 CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE II ISOFORM GAMMA-E - SUS SCROFA (PIG), 334 aa (fragment).	1.00E-163	
445	cg43274709	941	GAAGATTAGAAGTGAGATTCCAAGG[G/A]GAATGGGGGACAATATGTGATGACG	G	A	Gly	Gly	SILENT-CODING	struct	Human Gene Homologous to SPTREMBL-ID:Q28910 MUCIN - BOS TAURUS (BOVINE), 600 aa (fragment).	3.90E-106	12
446	cg43051155	1016	CGTGCCGAAGCTCAGCACCCATGAC[A/C]GTGCCATTGCCCTCCTTGTCAAAGA	A	C	Thr	Thr	SILENT-CODING	struct	Human Gene Homologous to SWISSPROT-ID:P12829 MYOSIN LIGHT CHAIN 1, EMBRYONIC MUSCLE/ATRIAL ISOFORM - HOMO SAPIENS (HUMAN), 196 aa.	5.30E-103	17

447	cg42731508	1386	ACGGCTTCGTCAGCGCCGCCGAGCT[G/A]CGACACGTCATGACCCGGCTGGGGG	G	A	Leu	Leu	SILENT-CODING	struct	Human Gene Similar to SWISSPROT-ID:P27482 CALMODULIN-RELATED PROTEIN NB-1 (CALMODULIN-LIKE PROTEIN) (CLP) - HOMO SAPIENS (HUMAN), 148 aa.	8.10E-75	2
448	cg44014373	559	ATTCATTGTTCTGCCGCTCCAGTTC[G/A]TGGCGTAGCTGCGTCAGTTCCTCCT	G	A	His	His	SILENT-CODING	struct	Human Gene Similar to SPTREMBL-ID:Q07426 KERATIN - CARASSIUS AURATUS (GOLDFISH), 455 aa.	6.10E-70	17
449	cg43936426	1293	GCTCCAGGTTCCGGGGCAGGGCCGA[G/A]GGGACCTCTTCCAACTGGTTCTTCT	G	A	Pro	Pro	SILENT-CODING	struct	Human Gene Similar to SWISSPROT-ID:P50608 FIBROMODULIN PRECURSOR (FM) - MUS MUSCULUS (MOUSE), 376 aa.	5.60E-67	1 (1q32)
450	cg43933305	1781	ACACCTGGTTCGTGTGGCCCTTCAC[G/A]CGGAAGGAGTCGTTCTCCCCCGTCT	G	A	Arg	Arg	SILENT-CODING	struct	Human Gene Similar to SWISSPROT-ID:P46680 ACTIN INTERACTING PROTEIN 1 - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 615 aa.	3.50E-66	4
451	cg42522566	256	TAGCAGGGGGTCGGTTTGGCCAGGT[G/C]CACAGGTGTACAGAGAGGTCTACAG	G	C	Val	Val	SILENT-CODING	struct	Human Gene Similar to SWISSPROT-ID:P07313 MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (EC 2.7.1.117) (MLCK) - ORYCTOLAGUS CUNICULUS (RABBIT), 607 aa.	6.00E-55	
452	cg42522566	286	GGTGTACAGAGAGGTCTACAGGCCT[T/C]GCACTGGCAGCCAAGATCATCAAAG	T	C	Leu	Leu	SILENT-CODING	struct	Human Gene Similar to SWISSPROT-ID:P07313 MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (EC 2.7.1.117) (MLCK) - ORYCTOLAGUS CUNICULUS (RABBIT), 607 aa.	6.00E-55	
453	cg42522566	295	AGAGGTCTACAGGCCTTGCACTGGC[A/T]GCCAAGATCATCAAAGTGAAGAACG	A	T	Ala	Ala	SILENT-CODING	struct	Human Gene Similar to SWISSPROT-ID:P07313 MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (EC 2.7.1.117) (MLCK) - ORYCTOLAGUS CUNICULUS (RABBIT), 607 aa.	6.00E-55	

454	cg43977322	2051	CCACATCGATGC TCTCGGCAAAGG C[A/G]CTCGCCT CGGCCCGGAGG CCTGGCT	A	G	Ser	Ser	SILENT-CODING	struct	Human Gene Similar to SWISSPROT-ID:P37709 TRICHOHYALIN - ORYCTOLAGUS CUNICULUS (RABBIT), 1407 aa.	1.50E-52	16
455	cg43918310	227	TGAGTTCCCAGC AGCAGAAGCAG CC[C/T]TGCATCC CACCCCCTCAGC TTCAGC	C	T	Pro	Pro	SILENT-CODING	struct	Human Gene Similar to SWISSPROT-ID:P22528 CORNIFIN B (SMALL PROLINE-RICH PROTEIN IB) (SPR-IB) - HOMO SAPIENS (HUMAN), 89 aa.	4.00E-50	1 (1q21)
456	cg43918310	362	CTGAGCCCTGCC ACCCCAAAGTGC C[T/C]GAGCCCT GCCAGCCCAAG GTTCCAG	T	C	Pro	Pro	SILENT-CODING	struct	Human Gene Similar to SWISSPROT-ID:P22528 CORNIFIN B (SMALL PROLINE-RICH PROTEIN IB) (SPR-IB) - HOMO SAPIENS (HUMAN), 89 aa.	4.00E-50	1 (1q21)
457	cg43248320	2084	TGGTGCGCTTCC TGCACTCCTGGA C[C/G]AACCTCC GGCTGCAGACA CTGCCCC	C	G	Thr	Thr	SILENT-CODING	sulfotransferase	Human Gene SWISSPROT-ID:P52848 HEPARAN SULFATE N-DEACETYLASE/N-SULFOTRANSFERASE (EC 2.8.2.-) (N-HSST) (N-HEPARAN SULFATE SULFOTRANSFERASE) (GLUCOSAMINYL N- DEACETYLASE/N-SULFOTRANSFERASE) - HOMO SAPIENS (HUMAN), 882 aa.	0.00E+00	5 (5q32)
458	cg43999676	536	TTGGGTATACAG CACTCAGTGAAA C[G/C]GAGAGTC CACGTTTATTCT CCTCCC	G	C	Thr	Thr	SILENT-CODING	sulfotransferase	Human Gene SWISSPROT-ID:Q06520 ALCOHOL SULFOTRANSFERASE (EC 2.8.2.2) (HYDROXYSTEROID SULFOTRANSFERASE) (HST) (DEHYDROEPIANDROSTERONE SULFOTRANSFERASE) (DHEA-ST) (ST2) (ST2A3) - HOMO SAPIENS (HUMAN), 284 aa.	7.80E-157	2 (2q12)
459	cg43987111	1817	AGGAGTCTGAGA ACTTCGTGTATT T[G/C]CCCACAA GGGCAATAGAG CAGGTCT	G	C	Gly	Gly	SILENT-CODING	synthase	Human Gene SWISSPROT-ID:P17812 CTP SYNTHASE (EC 6.3.4.2) (UTP--AMMONIA LIGASE) (CTP SYNTHETASE) - HOMO SAPIENS (HUMAN), 591 aa.	0.00E+00	18 (1p34.1)

460	cg43971304	1192	TCTCCAACAAGG GTGCTGACGTCT T[C/T]CTGGAGG CATTGGCTCGGC TCAACT	C	T	Phe	Phe	SILENT-CODING	synthase	Human Gene SWISSPROT-ID:P13807 GLYCOGEN (STARCH) SYNTHASE, MUSCLE (EC 2.4.1.11) - HOMO SAPIENS (HUMAN), 737 aa.	0.00E+00	19 (19q13.3)
461	cg43971304	385	TGGGGCCGTAC ACGGAGCAGGG CGT[G/C]AGGAC CCAGGTGGAACT GCTGGAGG	G	C	Val	Val	SILENT-CODING	synthase	Human Gene SWISSPROT-ID:P13807 GLYCOGEN (STARCH) SYNTHASE, MUSCLE (EC 2.4.1.11) - HOMO SAPIENS (HUMAN), 737 aa.	0.00E+00	19 (19q13.3)
462	cg43948262	1222	GTCCTTCCTGCT GCAACCATGAGA A[G/A]ACCCTGG GGATCCTCCAGG TCTGGG	G	A	Val	Val	SILENT-CODING	synthase	Human Gene SWISSPROT-ID:P22102 PHOSPHORIBOSYLAMINE–GLYCINE LIGASE (EC 6.3.4.13) (GARS) (GLYCINAMIDE RIBONUCLEOTIDE SYNTHETASE) (PHOSPHORIBOSYLGLYCINAMIDE SYNTHETASE) / PHOSPHORIBOSYLFORMYLGLYCINAMIDINE CYCLO-LIGASE (EC 6.3.3.1) (AIRS) (PHOSPHORIBOSYL-AMINOIMIDAZOLE SYNTHETASE) (AIR SYNTHASE) / PHOSPHORIBOSYLGLYCINAMIDE FORMYLTRANSFERASE (EC 2.1.2.2) (GART) (GAR TRANSFORMYLASE) (5'-PHOSPHORIBOSYLGLYCINAMIDE TRANSFORMYLASE) - HOMO SAPIENS (HUMAN), 1010 aa.	0.00E+00	21 (21q22.1)
463	cg43918661	587	CTCTTTCTGGTC TTTGCTTTTGCAT [G/A]ATGTCCTGG AAGTTCTTCAGC AGTC	G	A	Ile	Ile	SILENT-CODING	synthase	Human Gene SWISSPROT-ID:P13196 5-AMINOLEVULINIC ACID SYNTHASE MITOCHONDRIAL PRECURSOR, NONSPECIFIC (EC 2.3.1.37) (DELTA-AMINOLEVULINATE SYNTHASE) (DELTA-ALA SYNTHETASE) (ALAS-H) - HOMO SAPIENS (HUMAN), 640 aa.	7.50E-173	3 (3p21.1)

464	cg43953338	1430	ATACTTTGATGG GTCTTCGTTACT G[C/T]AAGGAGA GAGGAGCTTTAA CTGTGG	C	T	Cys	Cys	SILENT-CODING	synthase	Human Gene Homologous to SWISSPROT-ID:P44708 GLUCOSAMINE--FRUCTOSE-6-PHOSPHATE AMINOTRANSFERASE (ISOMERIZING) (EC 2.6.1.16) (HEXOSEPHOSPHATE AMINOTRANSFERASE) (D-FRUCTOSE-6- PHOSPHATE AMIDOTRANSFERASE) (GFAT) (L-GLUTAMINE-D-FRUCTOSE-6-PHOSPHATE AMIDOTRANSFERASE) (GLUCOSAMINE-6-PHOSPHATE SYNTHASE) - HAEMOPHILUS INFLUENZAE, 609 aa.	3.10E-107	2 (2p13)
465	cg42721903	326	ACATCACGAAAA GGGAAGAATTCT C[T/C]CCGCTGA CGGCCAACCTCA TGAATT	T	C	Ser	Ser	SILENT-CODING	synthase	Human Gene Similar to SWISSPROT-ID:Q06647 ATP SYNTHASE OLIGOMYCIN SENSITIVITY CONFERRAL PROTEIN PRECURSOR, MITOCHONDRIAL (EC 3.6.1.34) (OSCP) - RATTUS NORVEGICUS (RAT), 213 aa.	7.40E-79	
466	cg42721903	389	ATGGTCGCCTAG GCAACACCCAG GG[C/T]GTCATCT CTGCCTTCTCCA CCATCA	C	T	Gly	Gly	SILENT-CODING	synthase	Human Gene Similar to SWISSPROT-ID:Q06647 ATP SYNTHASE OLIGOMYCIN SENSITIVITY CONFERRAL PROTEIN PRECURSOR, MITOCHONDRIAL (EC 3.6.1.34) (OSCP) - RATTUS NORVEGICUS (RAT), 213 aa.	7.40E-79	
467	cg43933068	695	ATTTGATCAGAT GACCATTGAGGA C[T/C]TGAATGAA GCTTTCCCAGAA ACCAA	T	C	Leu	Leu	SILENT-CODING	synthase	Human Gene Similar to SWISSPROT-ID:P13620 ATP SYNTHASE D CHAIN, MITOCHONDRIAL (EC 3.6.1.34) - BOS TAURUS (BOVINE), 160 aa.	1.90E-75	12

468	cg43968419	606	AGCATCGGCTGCGCCTGGTGGCCAC[T/C]GATGGGGCCTTTTCCATGGATGGCG	T	C	Thr	Thr	SILENT-CODING	synthase	Human Gene Similar to SWISSNEW-ID:P53556 8-AMINO-7-OXONONANOATE SYNTHASE (EC 2.3.1.47) (7-KETO-8-AMINO-PELARGONIC ACID SYNTHETASE) (7-KAP SYNTHETASE) (L-ALANINE--PIMELYL COA LIGASE) - BACILLUS SUBTILIS, 389 aa.\|pcls:SWISSPROT-ID:P53556 8-AMINO-7-OXONONANOATE SYNTHASE (EC 2.3.1.47) (7-KETO-8-AMINO-PELARGONIC ACID SYNTHETASE) (7-KAP SYNTHETASE) (L-ALANINE--PIMELYL COA LIGASE) - BACILLUS SUBTILIS, 389 aa.	9.90E-70	
469	cg43064068	1466	GAGAGGTGGTGAAGGCATTTGTGGT[C/A]CTGGCCTCGCAGTTCCTGTCCCATG	C	A	Val	Val	SILENT-CODING	synthase	Human Gene Similar to SWISSNEW-ID:P39062 ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL-COA SYNTHASE) - BACILLUS SUBTILIS, 572 aa.\|pcls:SWISSPROT-ID:P39062 ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL-COA SYNTHASE) - BACILLUS SUBTILIS, 572 aa.	7.40E-65	
470	cg44017251	1301	ACACACAGCGGCTGGAGTGCATCGA[C/T]AATGACGAGTGCGCCGATGAGGAAC	C	T	Asp	Asp	SILENT-CODING	tgf	Human Gene SPTREMBL-ID:O00508 LATENT TGF-BETA BINDING PROTEIN-4 - HOMO SAPIENS (HUMAN), 1587 aa.	6.5e-315	
471	cg43925970	1694	CTATGCACAGAGCACATAAGGTGAA[G/A]GTGGTGACTCCCAGAGAAGCGACCT	G	A	Thr	Thr	SILENT-CODING	tm7	Human Gene SPTREMBL-ID:O00348 PUTATIVE ENDOTHELIN RECEPTOR TYPE B-LIKE PROTEIN - HOMO SAPIENS (HUMAN), 613 aa.	0.00E+00	9

472	cg43925970	1937	TGATGCCGGTCCCGAAGATCACCAC[A/G]GACAGACACATGACAGCATAGGCTC	A	G	Ser	Ser	SILENT-CODING	tm7	Human Gene SPTREMBL-ID:O00348 PUTATIVE ENDOTHELIN RECEPTOR TYPE B-LIKE PROTEIN - HOMO SAPIENS (HUMAN), 613 aa.	0.00E+00	9
473	cg43925970	1952	AGATCACCACAGACAGACACATGAC[A/C]GCATAGGCTCCATAGGACTCCTGGG	A	C	Ala	Ala	SILENT-CODING	tm7	Human Gene SPTREMBL-ID:O00348 PUTATIVE ENDOTHELIN RECEPTOR TYPE B-LIKE PROTEIN - HOMO SAPIENS (HUMAN), 613 aa.	0.00E+00	9
474	cg43925970	1955	TCACCACAGACAGACACATGACAGC[A/G]TAGGCTCCATAGGACTCCTGGGTCA	A	G	Tyr	Tyr	SILENT-CODING	tm7	Human Gene SPTREMBL-ID:O00348 PUTATIVE ENDOTHELIN RECEPTOR TYPE B-LIKE PROTEIN - HOMO SAPIENS (HUMAN), 613 aa.	0.00E+00	9
475	cg36988276	638	TTCACAAGATTCATTCTCTCCAAAA[A/G]GTTTTACTTGACATTCAAGATAACA	A	G	Lys	Lys	SILENT-CODING	tm7	Human Gene SWISSPROT-ID:P23945 FOLLICLE STIMULATING HORMONE RECEPTOR PRECURSOR (FSH-R) (FOLLITROPIN RECEPTOR) - HOMO SAPIENS (HUMAN), 695 aa.	0.00E+00	2 (2p21)
476	cg43275892	1359	GAACCAGCAGCTACTAGGGAGAAGT[C/T]TGCAAGATGTCAAGGGCCAAGAAGT	C	T	Leu	Leu	SILENT-CODING	tm7	Human Gene SWISSPROT-ID:Q99572 P2X PURINOCEPTOR 7 (ATP RECEPTOR) (P2X7) (PURINERGIC RECEPTOR) (P2Z RECEPTOR) - HOMO SAPIENS (HUMAN), 595 aa.	0.00E+00	
477	cg40358719	1284	TGGCCGTCCTCTACTGCTTCCTCAA[C/T]GGGGAGGTGCAGCTGGAGGTTCAGA	C	T	Asn	Asn	SILENT-CODING	tm7	Human Gene SWISSPROT-ID:P47872 SECRETIN RECEPTOR PRECURSOR (SCT-R) - HOMO SAPIENS (HUMAN), 440 aa.	3.00E-242	2 (2q14.1)
478	cg41084924	1296	CCCACCACGGTCTCCACAGCACTCC[C/T]GACAGCCCCGCCAAACCAGAGAAGA	C	T	Pro	Pro	SILENT-CODING	tm7	Human Gene SWISSPROT-ID:P14416 D(2) DOPAMINE RECEPTOR - HOMO SAPIENS (HUMAN), 443 aa.	1.70E-241	11

479	cg41084924	1422	CCTCCCTCAAGACCATGAGCCGTAG[G/A]AAGCTCTCCCAGCAGAAGGAGAAGA	G	A	Arg	Arg	SILENT-CODING	tm7	Human Gene SWISSPROT-ID:P14416 D(2) DOPAMINE RECEPTOR - HOMO SAPIENS (HUMAN), 443 aa.	1.70E-241	11
480	cg43264978	1175	CCAAGCTCATCGATGCCTCCAGAGT[C/G]TCAGAGACGGAGTACTCTGCCTTGG	C	G	Val	Val	SILENT-CODING	tm7	Human Gene TREMBLNEW-ID:G2736282 G PROTEIN COUPLED RECEPTOR - HOMO SAPIENS (HUMAN), 362 aa.	1.40E-196	
481	cg43264978	1193	CCAGAGTCTCAGAGACGGAGTACTC[T/C]GCCTTGGAGCAGAACACCAAATGAT	T	C	Ser	Ser	SILENT-CODING	tm7	Human Gene TREMBLNEW-ID:G2736282 G PROTEIN COUPLED RECEPTOR - HOMO SAPIENS (HUMAN), 362 aa.	1.40E-196	
482	cg43264978	140	CCCGCCTCAGAACGATGGATCTGCA[C/T]CTCTTCGACTACTCAGAGCCAGGGA	C	T	His	His	SILENT-CODING	tm7	Human Gene TREMBLNEW-ID:G2736282 G PROTEIN COUPLED RECEPTOR - HOMO SAPIENS (HUMAN), 362 aa.	1.40E-196	
483	cg43264978	164	ACCTCTTCGACTACTCAGAGCCAGG[G/C]AACTTCTCGGACATCAGCTGGCCAT	G	C	Gly	Gly	SILENT-CODING	tm7	Human Gene TREMBLNEW-ID:G2736282 G PROTEIN COUPLED RECEPTOR - HOMO SAPIENS (HUMAN), 362 aa.	1.40E-196	
484	cg3001696	1274	GCCCAGACCCCAGCAGCTTCAGCCG[G/C]CCCCGCGAAGCCACGGCCCGCGAGC	G	C	Arg	Arg	SILENT-CODING	tm7	Human Gene SWISSPROT-ID:P41143 DELTA-TYPE OPIOID RECEPTOR (DOR-1) - HOMO SAPIENS (HUMAN), 372 aa.	2.10E-195	1 (1p36.1)
485	cg43967090	790	GGGCTAAATATTTTATGGTTTTATT[C/T]ATTTACTGTGTTCTCATGCTGTGTT	C	T	Phe	Phe	SILENT-CODING	tm7	Human Gene SWISSNEW-ID:O43194 PUTATIVE G PROTEIN-COUPLED RECEPTOR GPR39 - HOMO SAPIENS (HUMAN), 453 aa.	5.10E-195	2

486	cg43326635	770	ACTTCAACTTCTTTGTGTGGGTGCT[G/C]CCCCCGCTTCTCCTCATGGTCCTCA	G	C	Leu	Leu	SILENT-CODING	tm7	Human Gene SWISSPROT-ID:P30542 ADENOSINE A1 RECEPTOR - HOMO SAPIENS (HUMAN), 326 aa.	1.10E-173	1
487	cg40245117	1286	CATGCCAATTTGTTTCCGTCATGAG[A/G]ATGGACTACATGGTATACTTCAGCT	A	G	Arg	Arg	SILENT-CODING	tm7	Human Gene SWISSPROT-ID:P33765 ADENOSINE A3 RECEPTOR - HOMO SAPIENS (HUMAN), 318 aa.	1.50E-167	1 (1p21)
488	cg21411454	920	TCTACTGCAAGTTCCACAACTTCTT[C/T]CCCATCGCCGCTGTCTTCGCCAGTA	C	T	Phe	Phe	SILENT-CODING	tm7	Human Gene Similar to SPTREMBL-ID:Q94736 TACHYKININ-LIKE RECEPTOR - STOMOXYS CALCITRANS (STABLE FLY), 678 aa.	6.60E-78	2
489	cg42666032	1372	TGCTGGGCGTCCACGAAGTGGTCTT[C/T]GCCTTCGTGACGGACGAGCACGCCC	C	T	Phe	Phe	SILENT-CODING	tm7	Human Gene Similar to SWISSPROT-ID:P30083 VASOACTIVE INTESTINAL POLYPEPTIDE RECEPTOR 1 PRECURSOR (VIP-R-1) (PITUITARY ADENYLATE CYCLASE ACTIVATING POLYPEPTIDE TYPE II RECEPTOR) (PACAP TYPE II RECEPTOR) (PACAP-R-2) - RATTUS NORVEGICUS (RAT), 459 aa.	2.40E-75	17 (17q25)
490	cg38841806	111	CCAGCTGGCAGCTGGCACTGTGGGC[A/C]CCAGCCTACCTGGCCCTGGTGCTGG	A	C	Ala	Ala	SILENT-CODING	tm7	Human Gene Similar to SWISSPROT-ID:P30975 TACHYKININ-LIKE PEPTIDES RECEPTOR 99D (DTKR) - DROSOPHILA MELANOGASTER (FRUIT FLY), 519 aa.	2.10E-67	
491	cg1408914	663	AGGGGAAGTTTCTCTCAGTGTTTTA[C/T]ACAAATGAGGTACCCATGCTGAACC	C	T	Tyr	Tyr	SILENT-CODING	tm7	Human Gene Similar to SPTREMBL-ID:Q63395 OLFACTORY RECEPTOR - RATTUS NORVEGICUS (RAT), 309 aa.	2.00E-62	
492	cg1408914	675	TCTCAGTGTTTTACACAAATGAGGT[A/T]CCCATGCTGAACCCCTTCATCTACT	A	T	Val	Val	SILENT-CODING	tm7	Human Gene Similar to SPTREMBL-ID:Q63395 OLFACTORY RECEPTOR - RATTUS NORVEGICUS (RAT), 309 aa.	2.00E-62	

493	cg1408914	87	CCCCCAAAATGCTGATGAGCTTTAT[C/T]TCAGAGAGGAACATCATCTCCTTTC	C	T	Ile	Ile	SILENT-CODING	tm7	Human Gene Similar to SPTREMBL-ID:Q63395 OLFACTORY RECEPTOR - RATTUS NORVEGICUS (RAT), 309 aa.	2.00E-62	
494	cg43336100	168	CGGATGATTATGATCTCATGTATGT[A/G]AATTTGGACAACGAAATAGACAATG	A	G	Val	Val	SILENT-CODING	tnf	Human Gene SWISSPROT-ID:P26022 PENTAXIN-RELATED PROTEIN PTX3 PRECURSOR (TUMOR NECROSIS FACTOR- INDUCIBLE PROTEIN TSG-14) - HOMO SAPIENS (HUMAN), 381 aa.	2.20E-207	3 (3q25)
495	cg21138682	220	TTTTGCTGTGTATCTTCATAGAAGG[T/C]TGGACAAGATAGAAGATGAAAGGAA	T	C	Leu	Leu	SILENT-CODING	tnf	Human Gene Homologous to SWISSNEW-ID:P29965 CD40 LIGAND (CD40-L) (TNF-RELATED ACTIVATION PROTEIN) (TRAP) (T CELL ANTIGEN GP39) (CD154 ANTIGEN) - HOMO SAPIENS (HUMAN), 261 aa.\|pcls:SWISSPROT-ID:P29965 CD40 LIGAND (CD40-L) (TNF-RELATED ACTIVATION PROTEIN) (TRAP) (T CELL ANTIGEN GP39) (CD154 ANTIGEN) - HOMO SAPIENS (HUMAN), 261 aa.	3.60E-136	X (Xq26)
496	cg43335558	1143	TGCTGGTTCCAGCAAATGAAGGTGA[C/T]CCCACTGAGACTCTGAGACAGTGCT	C	T	Asp	Asp	SILENT-CODING	tnfreceptor	Human Gene Similar to TREMBLNEW-ID:G2653845 TNF RECEPTOR-RELATED RECEPTOR FOR TRAIL - HOMO SAPIENS (HUMAN), 386 aa.	5.50E-89	8
497	cg44027791	1440	TCTTGCCACAGTCGGGGATGTGGCA[A/C]ACGTGCTTCTTCTTGCCCTGCTCTC	A	C	Val	Val	SILENT-CODING	transcript factor	Human Gene SWISSPROT-ID:Q02086 TRANSCRIPTION FACTOR SP2 (KIAA0048) - HOMO SAPIENS (HUMAN), 606 aa.	0.00E+00	17

498	cg43934374	1459	TAGGAGCCCATGAAGGCTTGTCCCC[A/G]ACACCTTTCATGAACTCAAATCTGA	A	G	Pro	Pro	SILENT-CODING	transcript factor	Human Gene SWISSNEW-ID:Q99081 TRANSCRIPTION FACTOR HTF4 (TRANSCRIPTION FACTOR 12) (E-BOX-BINDING PROTEIN) (HEB) - HOMO SAPIENS (HUMAN), 682 aa.\|pcls:SWISSPROT-ID:Q99081 TRANSCRIPTION FACTOR HTF4 (TRANSCRIPTION FACTOR 12) (E-BOX-BINDING PROTEIN) (HEB) - HOMO SAPIENS (HUMAN), 682 aa.	0.00E+00	15 (15q21)
499	cg43921342	2556	TGGGATTCAGGTTCCGCTCTCGCAC[C/T]TGCTGCTCCAGCCCCAGGATGACCT	C	T	Gln	Gln	SILENT-CODING	transcript factor	Human Gene SWISSNEW-ID:P15923 TRANSCRIPTION FACTOR E2-ALPHA (IMMUNOGLOBULIN ENHANCER BINDING FACTOR E12) (TRANSCRIPTION FACTOR-3) (TCF-3) (TRANSCRIPTION FACTOR ITF-1) - HOMO SAPIENS (HUMAN), 654 aa.\|pcls:SWISSPROT-ID:P15923 TRANSCRIPTION FACTOR E2-ALPHA (IMMUNOGLOBULIN ENHANCER BINDING FACTOR E12) (TRANSCRIPTION FACTOR-3) (TCF-3) (TRANSCRIPTION FACTOR ITF-1) - HOMO SAPIENS (HUMAN), 654 aa.	0.00E+00	
500	cg44130900	1140	ATTTTCTGACATTTGATCCTATAGC[T/C]AAAATGGCAAAAACTGTTAAGTACG	T	C	Ala	Ala	SILENT-CODING	transcript factor	Human Gene SPTREMBL-ID:Q15574 TRANSCRIPTION FACTOR SL1 - HOMO SAPIENS (HUMAN), 556 aa (fragment).	7.5e-310	2
501	cg43321351	580	GCTCTGTCAGGCTCTCGGGGGTGGC[A/G]ATGGTGATGGTGTCGGCGGCAGCCG	A	G	Ile	Ile	SILENT-CODING	transcript factor	Human Gene SPTREMBL-ID:O00146 P120E4F TRANSCRIPTION FACTOR - HOMO SAPIENS (HUMAN), 783 aa.	1.00E-290	
502	cg43336856	861	CCTGGTAAGGGGGCACCATTGGCGG[T/C]CCCTGCCCATACGGGGGCATAGCAC	T	C	Gly	Gly	SILENT-CODING	transcript factor	Human Gene TREMBLNEW-ID:G2895870 ZINC FINGER TRANSCRIPTION FACTOR (ZNF207) - HOMO SAPIENS (HUMAN), 478 aa.	1.90E-265	

503	cg43129605	399	GGCCCGCGCTC GGCCGCCCGCC GGT[G/A]AAGCG GAGGCTGGACC TGGAAACTG	G	A	Val	Val	SILENT-CODING	transcript factor	Human Gene SWISSPROT-ID:Q01094 TRANSCRIPTION FACTOR E2F1 (E2F-1) (RETINOBLASTOMA BINDING PROTEIN 3) (RBBP-3) (PRB-BINDING PROTEIN E2F-1) (PBR3) (RETINOBLASTOMA-ASSOCIATED PROTEIN 1) (RBAP-1) - HOMO SAPIENS (HUMAN), 437 aa.	2.80E-232	20
504	cg43984259	1159	TGTTTCCGGACG AACTGCTGCTGC T[A/G]CTGTTGCT GCTGCTGCTGCT GCTGC	A	G	Ser	Ser	SILENT-CODING	transcript factor	Human Gene SWISSPROT-ID:Q16254 TRANSCRIPTION FACTOR E2F4 (E2F-4) - HOMO SAPIENS (HUMAN), 413 aa.	5.50E-211	16 (16q22.1)
505	cg43984259	1693	CTCCAGCAAAGC ATCTGCAGATGT C[C/T]TCATGAGT GACGTAGGCCAA ACAGC	C	T	Glu	Glu	SILENT-CODING	transcript factor	Human Gene SWISSPROT-ID:Q16254 TRANSCRIPTION FACTOR E2F4 (E2F-4) - HOMO SAPIENS (HUMAN), 413 aa.	5.50E-211	16 (16q22.1)
506	cg44028769	343	CCTTCTTGTCCC CCGAGCCTGTCA C[G/A]ATGTATTT GTTATTTCTGGA GATGT	G	A	Ile	Ile	SILENT-CODING	transcript factor	Human Gene Homologous to SWISSPROT-ID:O02482 TRANSCRIPTION FACTOR UNC-37 - CAENORHABDITIS ELEGANS, 612 aa.	4.60E-119	1
507	cg43918209	1268	GGTTGGGAAAG GCGCCCTCCGC TTG[C/G]GCCGG AGGGGGCTGCA GGCGATCGG	C	G	Ala	Ala	SILENT-CODING	transcript factor	Human Gene Homologous to SPTREMBL-ID:Q03827 TRANSCRIPTION FACTOR ETR101 - HOMO SAPIENS (HUMAN), 223 aa.	2.70E-115	19
508	cg43918942	2589	CTGATGACCTCC TTCACAGTCCTC C[G/T]GAAGTCAT GCATTCTGGCTG CAACC	G	T	Arg	Arg	SILENT-CODING	transcript factor	Human Gene Homologous to SPTREMBL-ID:Q20429 SIMILAR TO TRANSCRIPTION INITIATION FACTOR IIB - CAENORHABDITIS ELEGANS, 759 aa.	1.60E-103	14
509	cg43918942	2617	AGTCATGCATTC TGGCTGCAACCA G[A/G]AGCGCTG CTCCACAGAGGC CAGAGG	A	G	Leu	Leu	SILENT-CODING	transcript factor	Human Gene Homologous to SPTREMBL-ID:Q20429 SIMILAR TO TRANSCRIPTION INITIATION FACTOR IIB - CAENORHABDITIS ELEGANS, 759 aa.	1.60E-103	14

510	cg43918942	2629	TGGCTGCAACCA GAAGCGCTGCTC C[A/G]CAGAGGC CAGAGGGGCGC CGGCCTG	A	G	Cys	Cys	SILENT-CODING	transcript factor	Human Gene Homologous to SPTREMBL-ID:Q20429 SIMILAR TO TRANSCRIPTION INITIATION FACTOR IIB - CAENORHABDITIS ELEGANS, 759 aa.	1.60E-103	14
511	cg43918942	2638	CCAGAAGCGCT GCTCCACAGAG GCC[A/C]GAGGG GCGCCGGCCTG TGTGCATCC	A	C	Ser	Ser	SILENT-CODING	transcript factor	Human Gene Homologous to SPTREMBL-ID:Q20429 SIMILAR TO TRANSCRIPTION INITIATION FACTOR IIB - CAENORHABDITIS ELEGANS, 759 aa.	1.60E-103	14
512	cg43918942	2665	AGGGGCGCCGG CCTGTGTGCATC CA[A/G]TCCCGCT TCATCCTCTGCA GAAGCC	A	G	Asp	Asp	SILENT-CODING	transcript factor	Human Gene Homologous to SPTREMBL-ID:Q20429 SIMILAR TO TRANSCRIPTION INITIATION FACTOR IIB - CAENORHABDITIS ELEGANS, 759 aa.	1.60E-103	14
513	cg43918942	2683	GCATCCAATCCC GCTTCATCCTCT G[C/T]AGAAGCCT CAGGGCAGTCAT GGATA	C	T	Leu	Leu	SILENT-CODING	transcript factor	Human Gene Homologous to SPTREMBL-ID:Q20429 SIMILAR TO TRANSCRIPTION INITIATION FACTOR IIB - CAENORHABDITIS ELEGANS, 759 aa.	1.60E-103	14
514	cg43918942	2686	TCCAATCCCGCT TCATCCTCTGCA G[A/G]AGCCTCA GGGCAGTCATG GATACCT	A	G	Leu	Leu	SILENT-CODING	transcript factor	Human Gene Homologous to SPTREMBL-ID:Q20429 SIMILAR TO TRANSCRIPTION INITIATION FACTOR IIB - CAENORHABDITIS ELEGANS, 759 aa.	1.60E-103	14
515	cg43918942	2707	GCAGAAGCCTCA GGGCAGTCATG GA[T/C]ACCTCAT GGTTCTTCTCCC CAAATT	T	C	Val	Val	SILENT-CODING	transcript factor	Human Gene Homologous to SPTREMBL-ID:Q20429 SIMILAR TO TRANSCRIPTION INITIATION FACTOR IIB - CAENORHABDITIS ELEGANS, 759 aa.	1.60E-103	14
516	cg43918942	2713	GCCTCAGGGCA GTCATGGATACC TC[A/G]TGGTTCT TCTCCCCAAATT CCAGTA	A	G	His	His	SILENT-CODING	transcript factor	Human Gene Homologous to SPTREMBL-ID:Q20429 SIMILAR TO TRANSCRIPTION INITIATION FACTOR IIB - CAENORHABDITIS ELEGANS, 759 aa.	1.60E-103	14

517	cg43918942	2728	TGGATACCTCAT GGTTCTTCTCCC C[A/G]AATTCCAG TAGATGCGCAAA TCGTG	A	G	Phe	Phe	SILENT-CODING	transcript factor	Human Gene Homologous to SPTREMBL-ID:Q20429 SIMILAR TO TRANSCRIPTION INITIATION FACTOR IIB - CAENORHABDITIS ELEGANS, 759 aa.	1.60E-103	14
518	cg43918942	2749	CCCCAAATTCCA GTAGATGCGCAA A[T/G]CGTGGAAT ATACAGGCACGG GTCTA	T	G	Arg	Arg	SILENT-CODING	transcript factor	Human Gene Homologous to SPTREMBL-ID:Q20429 SIMILAR TO TRANSCRIPTION INITIATION FACTOR IIB - CAENORHABDITIS ELEGANS, 759 aa.	1.60E-103	14
519	cg43051067	1325	CAAACCTGCACA TCCACCAGCGAG T[A/T]CACACAGG AGAGAGGCCCTA CAAGT	A	T	Val	Val	SILENT-CODING	transcript factor	Human Gene Similar to SWISSNEW-ID:Q02975 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - RATTUS NORVEGICUS (RAT), 576 aa.\|pcls:SWISSPROT-ID:Q02975 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - RATTUS NORVEGICUS (RAT), 576 aa.	1.30E-91	
520	cg43129641	1228	AAATGGTGGCAG CAACAGGTTCAA C[C/T]GGTGGCTT TTTGGAAGGTGT CGTGA	C	T	Pro	Pro	SILENT-CODING	transcript factor	Human Gene Similar to TREMBLNEW-ID:G2896154 TRANSCRIPTION FACTOR GETS-1 - CARASSIUS AURATUS (GOLDFISH), 471 aa.	2.10E-83	1 (1q32)
521	cg43255753	1095	CCGAGGCCGAG AGCAAAGAGGA GCA[T/C]GGCCC CGAGGCCTGCG ACGCGGCCA	T	C	His	His	SILENT-CODING	transcript factor	Human Gene Similar to TREMBLNEW-ID:G2920821 TRANSCRIPTION FACTOR T-BOX 5 - HOMO SAPIENS (HUMAN), 518 aa.	4.70E-63	
522	cg42532030	319	ATAAATGTGATG AGTGTGGGAAAG C[C/T]TTCAGTCA GAGCTCAGATCT TATTA	C	T	Ala	Ala	SILENT-CODING	transcript factor	Human Gene Similar to SWISSNEW-ID:Q61751 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - MUS MUSCULUS (MOUSE), 572 aa.\|pcls:SWISSPROT-ID:Q61751 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - MUS MUSCULUS (MOUSE), 572 aa.	1.90E-57	

523	cg43946772	1709	ATCAATATTTAATATACTGGCTACC[A/C]GTTCTAATCAGGAAAAAAAATCTTG	A	C	Thr	Thr	SILENT-CODING	transferase	Human Gene SPTREMBL-ID:Q29121 UDP-GALNAC:POLYPEPTIDE ALFA-1,ON-ACETYLGALACTOSAMINYL TRANSFERASE - SUS SCROFA (PIG), 559 aa.	0.00E+00	18
524	cg43948635	2125	CTATTTTGTAGCCCAGCTCCGTCAG[G/T]GCCTCAGACAGAGCCCTGCAGTTGG	G	T	Ala	Ala	SILENT-CODING	transferase	Human Gene TREMBLNEW-ID:E347899 SERINE HYDROXYMETHYL TRANSFERASE - OVIS ARIES (SHEEP), 484 aa.	2.50E-238	17
525	cg43948635	2164	CCCTGCAGTTGGCCACCACCTGGTG[T/C]TGATAAACTTTAAATTCCAGAGTCA	T	C	Gln	Gln	SILENT-CODING	transferase	Human Gene TREMBLNEW-ID:E347899 SERINE HYDROXYMETHYL TRANSFERASE - OVIS ARIES (SHEEP), 484 aa.	2.50E-238	17
526	cg43948635	2203	ATTCCAGAGTCATAGCTTGCTTCAG[T/G]GCCACAGCAACCCCAGCAATGGCGT	T	G	Ala	Ala	SILENT-CODING	transferase	Human Gene TREMBLNEW-ID:E347899 SERINE HYDROXYMETHYL TRANSFERASE - OVIS ARIES (SHEEP), 484 aa.	2.50E-238	17
527	cg43948635	2248	TGGCGTGGTTGTGGGGACCTCCCTG[C/A]AGGCCAGGGAACACAGCAGAATTGA	C	A	Leu	Leu	SILENT-CODING	transferase	Human Gene TREMBLNEW-ID:E347899 SERINE HYDROXYMETHYL TRANSFERASE - OVIS ARIES (SHEEP), 484 aa.	2.50E-238	17
528	cg43948635	2269	CCTGCAGGCCAGGGAACACAGCAGA[A/G]TTGATAAGAGACTCCAGGTTGTACA	A	G	Asn	Asn	SILENT-CODING	transferase	Human Gene TREMBLNEW-ID:E347899 SERINE HYDROXYMETHYL TRANSFERASE - OVIS ARIES (SHEEP), 484 aa.	2.50E-238	17
529	cg43948635	2275	GGCCAGGGAACACAGCAGAATTGAT[A/G]AGAGACTCCAGGTTGTACAGAATCT	A	G	Leu	Leu	SILENT-CODING	transferase	Human Gene TREMBLNEW-ID:E347899 SERINE HYDROXYMETHYL TRANSFERASE - OVIS ARIES (SHEEP), 484 aa.	2.50E-238	17

530	cg43948635	2370	AAGATCATGCCAGCTCGGCAGCCTC[G/T]CAGGGTCTTGTGAGTGGTGGTGGTC	G	T	Arg	Arg	SILENT-CODING	transferase	Human Gene TREMBLNEW-ID:E347899 SERINE HYDROXYMETHYL TRANSFERASE - OVIS ARIES (SHEEP), 484 aa.	2.50E-238	17
531	cg43948635	2986	CCAAAACTGCTCGGCTGGCGAAATT[T/C]TCCGAGGCAATCAGCTCCAATCCAA	T	C	Glu	Glu	SILENT-CODING	transferase	Human Gene TREMBLNEW-ID:E347899 SERINE HYDROXYMETHYL TRANSFERASE - OVIS ARIES (SHEEP), 484 aa.	2.50E-238	17
532	cg43995237	830	TTACTTGATGCAACTGACTTGTAAT[A/T]GCCAGAAATCCTGTGCAACAATAGA	A	T	Ala	Ala	SILENT-CODING	transferase	Human Gene SWISSPROT-ID:P53611 GERANYLGERANYL TRANSFERASE TYPE II BETA SUBUNIT (EC 2.5.1.-) (RAB GERANYLGERANYLTRANSFERASE BETA SUBUNIT) (RAB GERANYL-GERANYLTRANSFERASE BETA SUBUNIT) (RAB GG TRANSFERASE) (RAB GGTASE) - HOMO SAPIENS (HUMAN), 331 aa.	1.40E-182	1
533	cg42879858	531	CACACGCTGTGGCTATTTTGTTTTA[C/T]ACATTGAACAGCAATGTTCATTCTG	C	T	Tyr	Tyr	SILENT-CODING	transferase	Human Gene Homologous to SWISSPROT-ID:Q93070 ECTO-ADP-RIBOSYLTRANSFERASE 4 (EC 2.4.2.31) (NAD(P)(+)–ARGININE ADP-RIBOSYLTRANSFERASE 4) (MONO(ADP-RIBOSYL) TRANSFERASE 4) - HOMO SAPIENS (HUMAN), 267 aa (fragment).	4.60E-143	
534	cg43933127	2359	GATTTTCTGCAATTTGTCCTGTAAG[G/A]AATGGAACATTGGCTGAATTGTGAA	G	A	Phe	Phe	SILENT-CODING	transport	Human Gene SWISSPROT-ID:P41541 GENERAL VESICULAR TRANSPORT FACTOR P115 (TRANSCYTOSIS ASSOCIATED PROTEIN) (TAP) - BOS TAURUS (BOVINE), 961 aa.	0.00E+00	4

535	cg43919796	1566	CAGAATTGCTAA AGCGCATCCTGG A[C/T]AGCAACAA GAGAGTACAAGA AGCTG	C	T	Asp	Asp	SILENT-CODING	transport	Human Gene SWISSNEW-ID:Q92973 IMPORTIN BETA-2 SUBUNIT (KARYOPHERIN BETA-2 SUBUNIT) (TRANSPORTIN) (M9 REGION INTERACTION PROTEIN) (MIP) - HOMO SAPIENS (HUMAN), 890 aa.\|pcls:SWISSPROT-ID:Q92973 IMPORTIN BETA-2 SUBUNIT (KARYOPHERIN BETA-2 SUBUNIT) (TRANSPORTIN) (M9 REGION INTERACTION PROTEIN) - HOMO SAPIENS (HUMAN), 890 aa.	0.00E+00	5
536	cg43053829	1294	TGCTCAGGTTGC CACCAGCCTCTG T[C/A]ACTTCGTG GGATAACCCAAG TTGCA	C	A	Val	Val	SILENT-CODING	transport	Human Gene SWISSPROT-ID:Q92887 CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER (MULTIDRUG RESISTANCE-ASSOCIATED PROTEIN 2) (CANALICULAR MULTIDRUG RESISTANCE PROTEIN) - HOMO SAPIENS (HUMAN), 1545 aa.\|pcls:SPTREMBL-ID:Q92887 CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER - HOMO SAPIENS (HUMAN), 1545 aa.	0.00E+00	10
537	cg43998978	1880	GGTCTGCACGC CCTTTCTGGTGG C[C/T]TGTGCAC ATTTGCCGTCTA CGTGAC	C	T	Leu	Leu	SILENT-CODING	transport	Human Gene SPTREMBL-ID:Q92798 CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER - HOMO SAPIENS (HUMAN), 1545 aa.	0.00E+00	16

538	cg42719351	1242	CAGGATCCCTGGTGCTGCTGTGCACC[T/C]TGTCTTATCCTCCTCGTCAAGATGC	T	C	Thr	Thr	SILENT-CODING	transport	Human Gene SWISSPROT-ID:Q06495 RENAL SODIUM-DEPENDENT PHOSPHATE TRANSPORT PROTEIN 2 (SODIUM/PHOSPHATE COTRANSPORTER 2) (NA(+)/PI COTRANSPORTER 2) (RENAL SODIUM PHOSPHATE TRANSPORT PROTEIN 2) (RENAL NA+-DEPENDENT PHOSPHATE COTRANSPORTER 2) - HOMO SAPIENS (HUMAN), 639 aa.	0.00E+00	5 (5q35)
539	cg43935986	1447	TCGTAAGGAGGGTGCTGCACTTGGG[G/T]GTGCAGATGCTGATGCTGAGCTGTG	G	T	Gly	Gly	SILENT-CODING	transport	Human Gene SPTREMBL-ID:Q28437 ABC-TRANSPORTER - GORILLA GORILLA GORILLA (LOWLAND GORILLA), 703 aa.	0.00E+00	6 (6p21.3)
540	cg43935986	2101	TATACACAGATGTAGGGGAGAAGGG[A/G]AGCCAGCTGGCTGCGGGACAGAAAC	A	G	Gly	Gly	SILENT-CODING	transport	Human Gene SPTREMBL-ID:Q28437 ABC-TRANSPORTER - GORILLA GORILLA GORILLA (LOWLAND GORILLA), 703 aa.	0.00E+00	6 (6p21.3)
541	cg43935986	2380	GACAGGACCTCTATTCCCGCCTGGT[G/T]CAGCAGCGGCTGATGGACTGAGGCC	G	T	Val	Val	SILENT-CODING	transport	Human Gene SPTREMBL-ID:Q28437 ABC-TRANSPORTER - GORILLA GORILLA GORILLA (LOWLAND GORILLA), 703 aa.	0.00E+00	6 (6p21.3)
542	cg44008864	597	CAATGAGGTTGGCTGGAGAATCAAA[T/C]TTAGCTACTACTCCTTTGTCCAGGA	T	C	Lys	Lys	SILENT-CODING	transport	Human Gene SWISSPROT-ID:Q63120 CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER (MULTIDRUG RESISTANCE-ASSOCIATED PROTEIN 2) (CANALICULAR MULTIDRUG RESISTANCE PROTEIN) - RATTUS NORVEGICUS (RAT), 1541 aa.\|pcls:SPTREMBL-ID:Q63120 ORGANIC ANION TRANSPORTER - RATTUS NORVEGICUS (RAT), 1541 aa.	0.00E+00	

543	cg43300953	371	TGGCGGGGACC CCGGAGCACCG CTG[T/C]CGAGT GCCGGACGCCG CGAACCTGA	T	C	Cys	Cys	SILENT-CODING	transport	Human Gene TREMBLNEW-ID:E1284850 PUTATIVE INTEGRAL MEMBRANE TRANSPORT PROTEIN - RATTUS NORVEGICUS (RAT), 557 aa.	1.60E-261	5
544	cg43300953	425	GCGCCTGGCGC AACAACAGTGTC CC[G/A]CTGCGG CTGCGGGACGG CCGCGAGG	G	A	Pro	Pro	SILENT-CODING	transport	Human Gene TREMBLNEW-ID:E1284850 PUTATIVE INTEGRAL MEMBRANE TRANSPORT PROTEIN - RATTUS NORVEGICUS (RAT), 557 aa.	1.60E-261	5
545	cg43964039	3102	GGGAGCCAAGC ACTGCTCCTCCC AC[G/A]GCCAGC ATGAGGCGACC CGTCAGCT	G	A	Ala	Ala	SILENT-CODING	transport	Human Gene SWISSPROT-ID:P11166 GLUCOSE TRANSPORTER TYPE 1, ERYTHROCYTE/BRAIN - HOMO SAPIENS (HUMAN), 492 aa.	1.60E-259	1
546	cg44011204	825	TGCTTCTCGACT CCGTACGGTCCA C[G/A]TAATTTTG GAGGAGTCCTG CCCCCA	G	A	Tyr	Tyr	SILENT-CODING	transport	Human Gene SWISSNEW-ID:Q15758 NEUTRAL AMINO ACID TRANSPORTER B(0) (ATB(0)) - HOMO SAPIENS (HUMAN), 541 aa.\|pcls:SWISSPROT-ID:Q15758 NEUTRAL AMINO ACID TRANSPORTER B - HOMO SAPIENS (HUMAN), 541 aa.\|pcls:SPTREMBL-ID:Q15758 NEUTRAL AMINO ACID TRANSPORTER B - HOMO SAPIENS (HUMAN), 541 aa.	6.90E-197	
547	cg43924839	1431	CCCACTGTAATT TGCTGAGTGTCC G[G/A]TTTAACAT TAAAACAGTGCA TAAAG	G	A	Asn	Asn	SILENT-CODING	transport	Human Gene SWISSPROT-ID:P78382 CMP-SIALIC ACID TRANSPORTER (CMP-SIA-TR) - HOMO SAPIENS (HUMAN), 337 aa.	1.60E-172	6
548	cg43298674	600	AAACAAAGTAGG GGGCAATGATGC T[G/C]CCCACTCT GGAGGCCGTGG ATGTGA	G	C	Gly	Gly	SILENT-CODING	transport	Human Gene Similar to TREMBLNEW-ID:E1284850 PUTATIVE INTEGRAL MEMBRANE TRANSPORT PROTEIN - RATTUS NORVEGICUS (RAT), 557 aa.	5.2E-64	5

549	cg42726186	827	CAGTTGGTTCATCCAACAGGAAAAT[C/T]TGAGGATCTCCTAAAATGGCAATCC	C	T	Gln	Gln	SILENT-CODING	transport	Human Gene Similar to SPTREMBL-ID:Q92473 ABC-C TRANSPORTER - HOMO SAPIENS (HUMAN), 1704 aa.	2.5E-60	17
550	cg43269525	3119	TATGAGCTCTTGGCAGCTTTTCAGG[A/C]GTACCCCACTGTTCAACTGTAAATG	A	C	Thr	Thr	SILENT-CODING	ubiquitin	Human Gene SWISSNEW-ID:Q92462 UBIQUITIN--PROTEIN LIGASE PUB1 (EC 6.3.2.-) - SCHIZOSACCHAROMYCES POMBE (FISSION YEAST), 767 aa.	6.5E-163	15
551	cg43291895	321	ATCTATACAACTGGGAGGTGGCCAT[C/T]TTCGGGCCCCCCAACACCTACTACG	C	T	Ile	Ile	SILENT-CODING	ubiquitin	Human Gene Homologous to SWISSPROT-ID:P49427 UBIQUITIN-CONJUGATING ENZYME E2-32 KD COMPLEMENTING (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2-CDC34) - HOMO SAPIENS (HUMAN), 236 aa.	3.5E-129	
552	cg43120117	1162	TTGTAGATCATAATAACCGAACAAC[G/C]CAGTTGACAGACCCAAGGTTACACC	G	C	Thr	Thr	SILENT-CODING	ubiquitin	Human Gene Homologous to SWISSPROT-ID:P39940 UBIQUITIN--PROTEIN LIGASE RSP5 (EC 6.3.2.-) - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 809 aa.	7.00E-121	
553	cg44005525	795	TCCACTGTCTGGCCATTCTGTCATG[C/T]TCTGCTCTGTTGGTCATATACTGAG	C	T	Glu	Glu	SILENT-CODING	ubiquitin	Human Gene Homologous to SWISSPROT-ID:P51965 UBIQUITIN-CONJUGATING ENZYME E2-21 KD UBCH6 (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) - HOMO SAPIENS (HUMAN), 193 aa.	3.30E-101	
554	cg43921266	1300	CCCCCGAGCTGCTGCAGTGGGAGCC[G/A]TGGTGGTGATGGAGCAGGTCATCTC	G	A	His	His	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P02545 LAMIN A (70 KD LAMIN) - Homo sapiens (Human), 664 aa.	0.00E+00	1

555	cg43929067	1982	CCTCCGGGGGT GAGGAATCTGAA GA[G/C]GACTGG GTTGGAGGCAG CACAAGAC	G	C	Ser	Ser	SILENT-CODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75152 KIAA0663 PROTEIN - HOMO SAPIENS (HUMAN), 810 aa.	0.00E+00	1
556	cg43944666	1082	TTCTAGGGGTTC CTAAACCAAAAG A[G/A]TCTACAAC TGGGTTGCTGAA AGCCA	G	A	Glu	Glu	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:O15228 DIHYDROXYACETONE PHOSPHATE ACYLTRANSFERASE (EC 2.3.1.42) (DAP-AT) (GLYCERONE-PHOSPHATE O-ACYLTRANSFERASE) - Homo sapiens (Human), 680 aa.	0.00E+00	1
557	cg43947011	1749	TCTTCTCCAATG TGGCCAGGAGAT C[T/C]TCCACCTG GTTCCGTACAGA CTCAT	T	C	Glu	Glu	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q92542 HYPOTHETICAL PROTEIN KIAA0253 - Homo sapiens (Human), 708 aa (fragment).	0.00E+00	1
558	cg43948542	3513	ATCCTGCATATG CAAAATGGGTAC A[G/A]TCACACAG AGACCTGCCCAT CAAGC	G	A	Gln	Gln	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P07814 MULTIFUNCTIONAL AMINOACYL-TRNA SYNTHETASE [INCLUDES: GLUTAMYL-TRNA SYNTHETASE (EC 6.1.1.17) (GLUTAMATE--TRNA LIGASE); PROLYL-TRNA SYNTHETASE (EC 6.1.1.15) (PROLINE--TRNA LIGASE)] - Homo sapiens (Human), 1440 aa.	0.00E+00	1
559	cg43969426	2856	AGAAGATCTTCG ATGGGTCCCTAC A[G/A]CCACAAGA TGTTATGTGTAG CATAG	G	A	Gln	Gln	SILENT-CODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O15463 PTPL1-ASSOCIATED RHOGAP - HOMO SAPIENS (HUMAN), 1261 aa.	0.00E+00	1
560	cg43273361	1765	TCAAGAGCAGCT CCTGAGCCCTTC C[A/G]AGAGCAA AGACAGGAATGA GACCCC	A	G	Leu	Leu	SILENT-CODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:P79101 CLEAVAGE AND POLYADENYLATION SPECIFITY FACTOR PROTEIN - BOS TAURUS (BOVINE), 684 aa.	0.00E+00	2

561	cg43961763	550	CCCTTCCCTTTTCTGCCTTTTCTTG[G/A]TTGAGGTATTCCAGCACTTTCATTA	G	A	Asn	Asn	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P13521 SECRETOGRANIN II PRECURSOR (SGII) (CHROMOGRANIN C) - Homo sapiens (Human), 617 aa.	0.00E+00	2
562	cg44911887	797	CAAGATCTGGAAAAAAGCAAAAAAA[A/G]AAAACTTTAGCTGAAATCAACCAAA	A	G	Lys	Lys	SILENT-CODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q99728 BRCA1-ASSOCIATED RING DOMAIN PROTEIN - HOMO SAPIENS (HUMAN), 777 aa.	0.00E+00	2
563	cg43925942	2262	ACATATTTGATAAACTTAAAGAGGC[T/C]GTTAAGGAAGAAAGTATTAAACGAC	T	C	Ala	Ala	SILENT-CODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O60313 KIAA0567 PROTEIN - HOMO SAPIENS (HUMAN), 978 aa (fragment).	0.00E+00	3
564	cg43931104	1483	AGGATGAAGAGGACACTTGTCTGGA[T/C]TGCATACTGCACACAGGATCCATCG	T	C	Gln	Gln	SILENT-CODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75329 ATAXIN-7 - HOMO SAPIENS (HUMAN), 892 aa.	0.00E+00	3
565	cg43939697	947	GATACCAAGGTCCTACCAAGATGAC[A/G]AAAGAAGAGTTAAATGCCCTCAAGT	A	G	Thr	Thr	SILENT-CODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75766 TRIP PROTEIN - HOMO SAPIENS (HUMAN), 784 aa.	0.00E+00	3
566	cg43940975	304	CCTGATGGCTGTCTGGATCCACGGA[G/A]AAATATCCAAGACGCTCAAACTGGA	G	A	Phe	Phe	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P47897 GLUTAMINYL-TRNA SYNTHETASE (EC 6.1.1.18) (GLUTAMINE--TRNA LIGASE) (GLNRS) - Homo sapiens (Human), 775 aa.	0.00E+00	3
567	cg43948629	1640	TGCCTGTGACCCTGCCCAACATCGC[A/G]TCTTTCACTGGCAAGGGAGGCCCCC	A	G	Ala	Ala	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:Q15031 PROBABLE LEUCYL-TRNA SYNTHETASE, MITOCHONDRIAL PRECURSOR (EC 6.1.1.4) (LEUCINE--TRNA LIGASE) (LEURS) (KIAA0028) - Homo sapiens (Human), 903 aa.	0.00E+00	3

568	cg43948629	3577	CCTGTCCTCCCC AACCCCAGCTGG A[C/T]GTGCCTCC CAGGCCTGCTGT GGTTC	C	T	Asp	Asp	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:Q15031 PROBABLE LEUCYL-TRNA SYNTHETASE, MITOCHONDRIAL PRECURSOR (EC 6.1.1.4) (LEUCINE--TRNA LIGASE) (LEURS) (KIAA0028) - Homo sapiens (Human), 903 aa.	0.00E+00	3
569	cg43978862	955	AGTCCTTGACAG TGAACTTCATCA T[A/G]CAGCTGAA TGTGCATGCCAC AGCTG	A	G	Cys	Cys	SILENT-CODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAD43020 COAT PROTEIN GAMMA-COP - HOMO SAPIENS (HUMAN), 874 aa.	0.00E+00	3
570	cg43930961	2098	CGGTGGAAAACC CTTGGGACTGAT A[G/A]GGGGCGA GGCGCGGGTCA GACTCGT	G	A	Pro	Pro	SILENT-CODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:BAA20772 KIAA0313 PROTEIN - HOMO SAPIENS (HUMAN), 1499 aa.	0.00E+00	4
571	cg43935402	9617	CTCCTCCGGATC CCCAACTTTTGG T[T/C]TCAGAATC CAGCCAGAGGA CAGACC	T	C	Val	Val	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:Q03164 ZINC FINGER PROTEIN HRX (ALL-1) (TRITHORAX-LIKE PROTEIN) - Homo sapiens (Human), 3969 aa.	0.00E+00	4
572	cg43994452	954	CGATCTTCACGT GCCGCCTGGTG GG[C/T]GAGAGC TGGGCCATGCA GTTGAGGC	C	T	Ser	Ser	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:O76024 WOLFRAMIN - Homo sapiens (Human), 890 aa.	0.00E+00	4
573	cg43933355	1161	TGTATGAGCGCA GCATAGACCTGG G[A/G]CGGCCCA CTCTCCTGTCGT CAAAGT	A	G	Arg	Arg	SILENT-CODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q92608 MYELOBLAST KIAA0209 - HOMO SAPIENS (HUMAN), 1842 aa (fragment).	0.00E+00	5
574	cg43964609	678	TGACCACGTAGA AGCTGGAGCTCT C[C/T]TGGTAGCC AAAGATAAAGCC TGCAT	C	T	Gln	Gln	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P35443 THROMBOSPONDIN 4 PRECURSOR - Homo sapiens (Human), 961 aa.	0.00E+00	5

575	cg43981461	3634	TGTATCTGAAAA TGCTAATTACCT G[A/C]GAACACC AAGAACTCTTGT GGAACA	A	C	Arg	Arg	SILENT-CODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O43314 KIAA0433 - HOMO SAPIENS (HUMAN), 1243 aa.	0.00E+00	5
576	cg43999670	3571	AAGTGGAAATGG CTCAGAGGAGTG A[A/G]GAGAATGT GCTAGCACTGAA GAGCG	A	G	Glu	Glu	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q12766 HYPOTHETICAL PROTEIN KIAA0194 - Homo sapiens (Human), 1435 aa (fragment).	0.00E+00	5
577	cg43918386	304	GACTGGAAGGAT GGTGGCTGTGCT C[A/G]TTACACGG TCGGCAAGGCAT TGTCC	A	G	Ser	Ser	SILENT-CODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q14511 ENHANCER OF FILMENTATION 1 - HOMO SAPIENS (HUMAN), 834 aa.	0.00E+00	6
578	cg43925091	2303	CTAGAACAGAGG TGGAGGAGGCG CC[G/T]GCGGTC CTCTGCCATGTC CCGGCTC	G	T	Arg	Arg	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q14999 HYPOTHETICAL PROTEIN KIAA0076 (HA0936) - Homo sapiens (Human), 1698 aa.	0.00E+00	6
579	cg43932558	1823	TCACCCTGATGG GATTCATGTCGG G[C/T]CGACTAG GCTTGGAAACGG CTTTCA	C	T	Arg	Arg	SILENT-CODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q14670 MRNA (KIAA0082) FOR ORF (NOVEL PROTEIN) - HOMO SAPIENS (HUMAN), 607 aa (fragment).	0.00E+00	6
580	cg43968933	1726	AGAAAACTGCTA AATCAAAAAAAA A[A/G]AAAACTTT AAAAAAAAAACC TACAC	A	G	Lys	Lys	SILENT-CODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:CAB46275 SEC63 PROTEIN - HOMO SAPIENS (HUMAN), 759 aa.	0.00E+00	6
581	cg43971946	4582	CCTCCTCTTCTT CATCGATCTCAA A[T/C]GTGGGTTC TAATCTTGGCAT TGGCC	T	C	Thr	Thr	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q92794 MONOCYTIC LEUKEMIA ZINC FINGER PROTEIN - Homo sapiens (Human), 2004 aa.	0.00E+00	8

582	cg43916922	5946	AGTCCTGCAGCA GACGAGCTTCCC G[A/G]AATTTGTA CTCCTTGATGTC ATCCC	A	G	Phe	Phe	SILENT-CODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75181 KIAA0699 PROTEIN - HOMO SAPIENS (HUMAN), 847 aa (fragment).	0.00E+00	9
583	cg43921541	1233	CATGGTAGGCAT CCAGGAGCCCTT G[C/T]CGGTCTC CAGAGTCGTAAA TTGCAT	C	T	Arg	Arg	SILENT-CODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:CAA10753 TIP ASSOCIATING PROTEIN - HOMO SAPIENS (HUMAN), 619 aa.	0.00E+00	11
584	cg43966967	2002	CTGCCGGCCCA GCCTCCTTCTGC TG[C/T]CACATGT TCTGGTGCGAGC CCAATG	C	T	Cys	Cys	SILENT-CODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O00213 STAT-LIKE PROTEIN - HOMO SAPIENS (HUMAN), 710 aa.	0.00E+00	11
585	cg43329920	1900	AGAGCCGGGCC CTCGGGGGTCC TCC[A/T]GAATAC CTGGGACAAAGA CACAGGC	A	T	Pro	Pro	SILENT-CODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q16538 PROTEIN A-2 - HOMO SAPIENS (HUMAN), 588 aa.	0.00E+00	12
586	cg43329920	1903	GCCGGGCCCTC GGGGGTCCTCC AGA[A/G]TACCTG GGACAAAGACAC AGGCTGG	A	G	Glu	Glu	SILENT-CODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q16538 PROTEIN A-2 - HOMO SAPIENS (HUMAN), 588 aa.	0.00E+00	12
587	cg43329920	1925	AGAATACCTGGG ACAAAGACACAG G[C/T]TGGAGGA CGAGGAGGACG AGGAAGA	C	T	Leu	Leu	SILENT-CODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q16538 PROTEIN A-2 - HOMO SAPIENS (HUMAN), 588 aa.	0.00E+00	12
588	cg43334182	5043	GAGGCAAGACTT GTGGAGCTTGAG G[T/C]TGACTCAC TGGCTGTGCAGT AGTGG	T	C	Gln	Gln	SILENT-CODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O15052 KIAA0344 - HOMO SAPIENS (HUMAN), 1246 aa.	0.00E+00	12

589	cg43916884	404	GCTGATGATGGTCCTTAGGTTTCAG[G/A]GTGGCCTGAGTCTTGGATGGGGATA	G	A	Thr	Thr	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P46087 PROLIFERATING-CELL NUCLEOLAR ANTIGEN P120 (PROLIFERATION-ASSOCIATED NUCLEOLAR PROTEIN P120) - Homo sapiens (Human), 855 aa.	0.00E+00	12
590	cg43918356	2336	CGCTACGTCCTATATTTTGCAAATT[T/C]AGTTTATCAAACTCAACAGTCAAAT	T	C	Leu	Leu	SILENT-CODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75176 KIAA0692 PROTEIN - HOMO SAPIENS (HUMAN), 783 aa (fragment).	0.00E+00	12
591	cg43918566	1480	AGGCTGGCATGGAGCGGGAACTGGA[G/A]AACATCATCCAGGAGACAGAGAAAG	G	A	Glu	Glu	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q13438 PROTEIN OS-9 PRECURSOR - Homo sapiens (Human), 667 aa.	0.00E+00	12
592	cg43918566	808	TCCGGCCCCCACCCAGTGCTGCACC[G/A]CAGGCCATCCTCTGTCACCCTTCCC	G	A	Pro	Pro	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q13438 PROTEIN OS-9 PRECURSOR - Homo sapiens (Human), 667 aa.	0.00E+00	12
593	cg43950437	955	GCTTGGCCCCACGTCGCAGCTTGCC[C/T]ACAACTGACAAAAAAGCACTGAAGA	C	T	Val	Val	SILENT-CODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q15021 ORF - HOMO SAPIENS (HUMAN), 1401 aa.	0.00E+00	12
594	cg43969319	1996	GATTACCAGATTTAATTGAAGAAAA[C/T]CATGTTGTAAATAAGACAGACTTGA	C	T	Asn	Asn	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q15398 HYPOTHETICAL PROTEIN KIAA0008 - Homo sapiens (Human), 765 aa.	0.00E+00	14
595	cg44018598	1379	ATTTACTTGAATTGTCTAGGACAGG[A/G]AGATCTTCACTATCACTGCTTTGTC	A	G	Leu	Leu	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P29374 RETINOBLASTOMA BINDING PROTEIN 1 (RBBP-1) - Homo sapiens (Human), 1257 aa.	0.00E+00	14

596	cg44018598	953	AAGGTAGAGAAA ATGTTTATCACC T[A/G]CATTCTAC AGCAAGTACATT TTGTG	A	G	Cys	Cys	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P29374 RETINOBLASTOMA BINDING PROTEIN 1 (RBBP-1) - Homo sapiens (Human), 1257 aa.	0.00E+00	14
597	cg44018598	986	CAGCAAGTACAT TTTGTGGGGGAG A[C/T]GATGATGA GGGACTCATTCC AGTGT	C	T	Ser	Ser	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P29374 RETINOBLASTOMA BINDING PROTEIN 1 (RBBP-1) - Homo sapiens (Human), 1257 aa.	0.00E+00	14
598	cg44022133	3061	AATGGCCCCAGT CCAATCCCAAAT T[T/C]CTTTGTGC TGACTATGCCGA GCAAG	T	C	Phe	Phe	SILENT-CODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75158 KIAA0670 PROTEIN - HOMO SAPIENS (HUMAN), 1280 aa (fragment).	0.00E+00	14
599	cg43981471	3033	CCCAGCCTCCTG AGGGCCCTGGC CT[C/T]CCGAGG AGATCACCCCTC ATTCGTA	C	T	Leu	Leu	SILENT-CODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O15082 KIAA0377 - HOMO SAPIENS (HUMAN), 1406 aa.	0.00E+00	15
600	cg43926221	5853	GCACCGAGAAA GTCGGTTGTATC TG[C/T]TGAATTT GTCTGTTTTTATT AGTAC	C	T	Gln	Gln	SILENT-CODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O15025 KIAA0308 - HOMO SAPIENS (HUMAN), 1297 aa (fragment).	0.00E+00	16
601	cg43945577	1886	TCACTTCCTCTG AATACCTTCCTA C[G/A]TTATGGGT CAAGCTTTACAA AAGCG	G	A	Thr	Thr	SILENT-CODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q15155 PM5 PROTEIN - HOMO SAPIENS (HUMAN), 1190 aa.	0.00E+00	16
602	cg43945577	1988	TCCATTTCCCCC CACTGCTCAGAG A[T/C]GGCGAGA ACTATGTTGTGC TTCTGG	T	C	Asp	Asp	SILENT-CODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q15155 PM5 PROTEIN - HOMO SAPIENS (HUMAN), 1190 aa.	0.00E+00	16

603	cg43955093	2884	GGGGCTGTGGGGGCATCCGCCCAGG[T/C]GTCCCTCCATCAGAGGGGCTATCAT	T	C	Thr	Thr	SILENT-CODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q16084 P130 - HOMO SAPIENS (HUMAN), 1139 aa.	0.00E+00	16
604	cg43983241	362	AGTGTGACACAATATTCACTTTTGT[G/C]GAAAAAAATGTTGCTACTTGGAAAT	G	C	Val	Val	SILENT-CODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q15219 PROTEIN P84 - HOMO SAPIENS (HUMAN), 657 aa.	0.00E+00	18
605	cg43983241	395	ATGTTGCTACTTGGAAATCAAATAC[A/C]TTCTATTCTGCTGGGAAAAATTACT	A	C	Thr	Thr	SILENT-CODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q15219 PROTEIN P84 - HOMO SAPIENS (HUMAN), 657 aa.	0.00E+00	18
606	cg42702030	2347	TACAGTGCGGGCACAAGAAGCTGCA[G/A]GGCCGCCTGCAGCTGTTCGGCCAGG	G	A	Gln	Gln	SILENT-CODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q92619 MYELOBLAST KIAA0223 - HOMO SAPIENS (HUMAN), 1165 aa (fragment).	0.00E+00	19
607	cg43297500	1921	GGGCCTTCCAGACAGTCGTGCTGGA[T/C]CCTGAAGGGGATGCCCAGATCGATC	T	C	Asp	Asp	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P49747 CARTILAGE OLIGOMERIC MATRIX PROTEIN PRECURSOR (COMP) - Homo sapiens (Human), 757 aa.	0.00E+00	19
608	cg43927434	3540	AGCAGGCCTCCTGTAGCTCGCTAAT[G/T]ACCCGTGACTTTACCATCCACTGCA	G	T	Val	Val	SILENT-CODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q92797 SYMPLEKIN - HOMO SAPIENS (HUMAN), 1142 aa.	0.00E+00	19
609	cg43927434	606	GAGGGGGCCGGGGTGCTGGGGCCGG[C/G]GCCAAGGTCAGGGGCTCCAGATCAT	C	G	Ala	Ala	SILENT-CODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q92797 SYMPLEKIN - HOMO SAPIENS (HUMAN), 1142 aa.	0.00E+00	19

610	cg43991657	193	CCAGGGCAGCC GCTGCAGCAGC AGA[C/G]GAGCG GGAAGGTGTGG CCACAGCTT	C	G	Ser	Ser	SILENT-CODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75807 APOPTOSIS ASSOCIATED PROTEIN - HOMO SAPIENS (HUMAN), 674 aa.	0.00E+00	19
611	cg43991657	208	CAGCAGCAGAC GAGCGGGAAGG TGT[G/A]GCCACA GCTTGGCTCAAG GGCGTGG	G	A	Ala	Ala	SILENT-CODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75807 APOPTOSIS ASSOCIATED PROTEIN - HOMO SAPIENS (HUMAN), 674 aa.	0.00E+00	19
612	cg43919691	1039	TCTTCATTTCACT CAACTGCTGCCT [G/A]ACCAGGGC AAGCTCATCGCT CTGTT	G	A	Val	Val	SILENT-CODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75300 ES/130 - HOMO SAPIENS (HUMAN), 977 aa.	0.00E+00	20
613	cg43936220	1966	TCTGCGTGCTCA TCTCCCGGCTCG C[A/G]GCCTCGA AGGGCTTTAGCG CACGGC	A	G	Ala	Ala	SILENT-CODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75132 KIAA0637 PROTEIN - HOMO SAPIENS (HUMAN), 1171 aa.	0.00E+00	22
614	cg43973809	1170	TCGTGGCTGTGG TCTTCCAGGATG A[G/A]AACACTCC TTTCGTGCCCGA CATGA	G	A	Glu	Glu	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P47736 RAP1 GTPASE ACTIVATING PROTEIN 1 (RAP1GAP) - Homo sapiens (Human), 663 aa.	0.00E+00	1 (1p36.1)
615	cg17663981	207	AAGATGGCTCTG GGGATCCCGAG AA[C/T]CCGGGC ACAGCGAGAGC CTGGTGCC	C	T	Asn	Asn	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q05329 GLUTAMATE DECARBOXYLASE, 65 KD ISOFORM (EC 4.1.1.15) (GAD-65) (65 KD GLUTAMIC ACID DECARBOXYLASE) - Homo sapiens (Human), 585 aa.	0.00E+00	10 (10p11.23)
616	cg17663981	210	ATGGCTCTGGG GATCCCGAGAAC CC[G/C]GGCACA GCGAGAGCCTG GTGCCAAG	G	C	Pro	Pro	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q05329 GLUTAMATE DECARBOXYLASE, 65 KD ISOFORM (EC 4.1.1.15) (GAD-65) (65 KD GLUTAMIC ACID DECARBOXYLASE) - Homo sapiens (Human), 585 aa.	0.00E+00	10 (10p11.23)

617	cg17663981	220	GGATCCCGAGAACCCGGGCACAGCG[A/C]GAGCCTGGTGCCAAGTGGCCCAAAA	A	C	Arg	Arg	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q05329 GLUTAMATE DECARBOXYLASE, 65 KD ISOFORM (EC 4.1.1.15) (GAD-65) (65 KD GLUTAMIC ACID DECARBOXYLASE) - Homo sapiens (Human), 585 aa.	0.00E+00	10 (10p11.23)
618	cg17663981	240	CAGCGAGAGCCTGGTGCCAAGTGGC[C/T]CAAAAGTTCACGGGCGGCATCGGAAACA	C	T	Ala	Ala	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q05329 GLUTAMATE DECARBOXYLASE, 65 KD ISOFORM (EC 4.1.1.15) (GAD-65) (65 KD GLUTAMIC ACID DECARBOXYLASE) - Homo sapiens (Human), 585 aa.	0.00E+00	10 (10p11.23)
619	cg17663981	243	CGAGAGCCTGGTGCCAAGTGGCCCA[A/G]AAGTTCACGGGCGGCATCGGAAACA	A	G	Gln	Gln	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q05329 GLUTAMATE DECARBOXYLASE, 65 KD ISOFORM (EC 4.1.1.15) (GAD-65) (65 KD GLUTAMIC ACID DECARBOXYLASE) - Homo sapiens (Human), 585 aa.	0.00E+00	10 (10p11.23)
620	cg17663981	372	GGAAGGCCGCCTGCACCTGCGACCA[A/G]AACCCTGCAGCTGCCCCAAAGGGG	A	G	Gln	Gln	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q05329 GLUTAMATE DECARBOXYLASE, 65 KD ISOFORM (EC 4.1.1.15) (GAD-65) (65 KD GLUTAMIC ACID DECARBOXYLASE) - Homo sapiens (Human), 585 aa.	0.00E+00	10 (10p11.23)
621	cg17663981	375	AGGCCGCCTGCACCTGCGACCAAAA[A/G]CCCTGCAGCTGCCCCAAAGGGGATG	A	G	Lys	Lys	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q05329 GLUTAMATE DECARBOXYLASE, 65 KD ISOFORM (EC 4.1.1.15) (GAD-65) (65 KD GLUTAMIC ACID DECARBOXYLASE) - Homo sapiens (Human), 585 aa.	0.00E+00	10 (10p11.23)
622	cg43968854	6834	TATGCACTGACAAGCCCACGACTC A[T/C]GAGAAAACTACCAAAATAGCCTGCA	T	C	His	His	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P46013 ANTIGEN KI-67 - Homo sapiens (Human), 3256 aa.	0.00E+00	10 (10q25)

623	cg43968854	9441	AAGAGGAACACA AATTACAAGACT C[G/A]GTCCCTG AAAATAAGGGAA TATCCC	G	A	Ser	Ser	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P46013 ANTIGEN KI-67 - Homo sapiens (Human), 3256 aa.	0.00E+00	10 (10q25)
624	cg43979900	2597	TGGCAAATTGTT GTGACACATTGA A[A/G]TAAGGAAG AAATGGCCGTAT GCACT	A	G	Tyr	Tyr	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P54803 GALACTOCEREBROSIDASE PRECURSOR (EC 3.2.1.46) (GALCERASE) (GALACTOSYLCERAMIDASE) (GALACTOSYLCERAMIDE BETA-GALACTOSIDASE) (GALACTOCEREBROSIDE BETA-GALACTOSIDASE) - Homo sapiens (Human), 669 aa.	0.00E+00	14 (14q24.3)
625	cg43979900	2816	CCACGTAGTGCC CACTCCATGGCT C[T/C]TGGGCCG TCATCAACCCGC ATCTCC	T	C	Gln	Gln	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P54803 GALACTOCEREBROSIDASE PRECURSOR (EC 3.2.1.46) (GALCERASE) (GALACTOSYLCERAMIDASE) (GALACTOSYLCERAMIDE BETA-GALACTOSIDASE) (GALACTOCEREBROSIDE BETA-GALACTOSIDASE) - Homo sapiens (Human), 669 aa.	0.00E+00	14 (14q24.3)
626	cg44014448	3469	TCCAGAAAGATT TGGTGAAGGAAG C[C/T]ATCAACTC CTATATCAGAGG GGACG	C	T	Ala	Ala	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P53675 CLATHRIN HEAVY CHAIN 2 (CLH-22) - Homo sapiens (Human), 1640 aa.	0.00E+00	17 (17q11)
627	cg44928323	3760	CAAGAGCTACAT TTATGGAAGTTC T[G/C]ACAAAAAT CCTTCAACAAGG CACAG	G	C	Leu	Leu	SILENT-CODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:P97526 NEUROFIBROMIN - RATTUS NORVEGICUS (RAT), 2820 aa.	0.00E+00	17 (17q11.2)

628	cg43973129	1228	AGCGCTATAGGG GCAGAGGAAGT GA[G/A]GAATACA GGGCTCCAAGA CCTCAGA	G	A	Glu	Glu	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P05060 SECRETOGRANIN I PRECURSOR (SGI) (CHROMOGRANIN B) - Homo sapiens (Human), 677 aa.	0.00E+00	20 (20pter)
629	cg43955813	1995	GTCATGATGAAA TTTCCAGATGTT C[G/A]CTGAGTG AGCCATTGGAAA GTGATG	G	A	Ser	Ser	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q03188 CENTROMERE PROTEIN C (CENP-C) (CENTROMERE AUTOANTIGEN C) - Homo sapiens (Human), 943 aa.	0.00E+00	4 (4q12)
630	cg44923983	576	GGAATTACAATT TTGGTGGAGAAT T[C/T]GTAGAAGC CATGATTCGTCA ACTTA	C	T	Phe	Phe	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q09161 80 KD NUCLEAR CAP BINDING PROTEIN (NCBP 80 KD SUBUNIT) (CBP80) - Homo sapiens (Human), 790 aa.	0.00E+00	9 (9q22.3)
631	cg25268354	1419	TCATCACCTCCT GCACGTACAACA C[G/A]GAAGACC GGGAGCTGGCC ACAGTGG	G	A	Thr	Thr	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P09172 DOPAMINE BETA-MONOOXYGENASE PRECURSOR (EC 1.14.17.1) (DOPAMINE BETA- HYDROXYLASE) (DBH) - Homo sapiens (Human), 603 aa.	0.00E+00	9 (9q34)
632	cg43921948	1765	AAGATCCCAGAG AGAGAAACCCAC T[A/T]ACTCCAGC ATCCGAGCCCC GGTTTT	A	T	Leu	Leu	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P08842 STERYL-SULFATASE PRECURSOR (EC 3.1.6.2) (STEROID SULFATASE) (STERYL- SULFATE SULFOHYDROLASE) (ARYLSULFATASE C) (ASC) - Homo sapiens (Human), 583 aa.	0.00E+00	X
633	cg43032555	677	GCTTTCTCGGCT TCTGACTGGTCC A[A/G]GATCTTCT GCCGCTCAAGC CGACCG	A	G	Leu	Leu	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q14764 MAJOR VAULT PROTEIN (MVP) (LUNG RESISTANCE-RELATED PROTEIN) - Homo sapiens (Human), 896 aa.	0.00E+00	
634	cg43032555	699	CCAAGATCTTCT GCCGCTCAAGC CG[A/G]CCGCGG GCTTCCTGTTCC AGTCTCT	A	G	Gly	Gly	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q14764 MAJOR VAULT PROTEIN (MVP) (LUNG RESISTANCE-RELATED PROTEIN) - Homo sapiens (Human), 896 aa.	0.00E+00	

635	cg43032555	714	GCTCAAGCCGAC CGCGGGCTTCCT G[T/C]TCCAGTCT CTGAGCCTCATG CTTGG	T	C	Glu	Glu	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q14764 MAJOR VAULT PROTEIN (MVP) (LUNG RESISTANCE-RELATED PROTEIN) - Homo sapiens (Human), 896 aa.	0.00E+00	
636	cg43032555	765	CCGCCGCTTCCT GGGAGTTGGTG GT[A/G]ATCTCGA TGGCCAGCTGAA CGCTGC	A	G	Ile	Ile	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q14764 MAJOR VAULT PROTEIN (MVP) (LUNG RESISTANCE-RELATED PROTEIN) - Homo sapiens (Human), 896 aa.	0.00E+00	
637	cg43032555	783	TGGTGGTAATCT CGATGGCCAGCT G[A/G]ACGCTGC GCTGAAGGGCAT CCCGGG	A	G	Val	Val	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q14764 MAJOR VAULT PROTEIN (MVP) (LUNG RESISTANCE-RELATED PROTEIN) - Homo sapiens (Human), 896 aa.	0.00E+00	
638	cg43032555	792	TCTCGATGGCCA GCTGAACGCTGC G[C/T]TGAAGGG CATCCCGGGTCC TCTGAT	C	T	Gln	Gln	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q14764 MAJOR VAULT PROTEIN (MVP) (LUNG RESISTANCE-RELATED PROTEIN) - Homo sapiens (Human), 896 aa.	0.00E+00	
639	cg43032555	795	CGATGGCCAGCT GAACGCTGCGCT G[A/C]AGGGCAT CCCGGGTCCTCT GATCCA	A	C	Leu	Leu	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q14764 MAJOR VAULT PROTEIN (MVP) (LUNG RESISTANCE-RELATED PROTEIN) - Homo sapiens (Human), 896 aa.	0.00E+00	
640	cg43032555	801	CCAGCTGAACGC TGCGCTGAAGG GC[A/G]TCCCGG GTCCTCTGATCC ACAGGCT	A	G	Asp	Asp	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q14764 MAJOR VAULT PROTEIN (MVP) (LUNG RESISTANCE-RELATED PROTEIN) - Homo sapiens (Human), 896 aa.	0.00E+00	
641	cg43032555	840	GATCCACAGGCT CCACTGACTGCA C[A/G]TCCACACT GCTGACTACCAG CCCGT	A	G	Asp	Asp	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q14764 MAJOR VAULT PROTEIN (MVP) (LUNG RESISTANCE-RELATED PROTEIN) - Homo sapiens (Human), 896 aa.	0.00E+00	

642	cg43032555	855	CTGACTGCACAT CCACACTGCTGA C[T/C]ACCAGCC CGTTTTGGGGAA AGACAG	T	C	Val	Val	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q14764 MAJOR VAULT PROTEIN (MVP) (LUNG RESISTANCE-RELATED PROTEIN) - Homo sapiens (Human), 896 aa.	0.00E+00	
643	cg43032555	873	TGCTGACTACCA GCCCGTTTTGGG G[A/G]AAGACAG CCTGGTCCCGG GGCCTGG	A	G	Phe	Phe	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q14764 MAJOR VAULT PROTEIN (MVP) (LUNG RESISTANCE-RELATED PROTEIN) - Homo sapiens (Human), 896 aa.	0.00E+00	
644	cg43054046	2616	TACTGGGTGTGA AAGCTGTTTTGG C[T/C]GAAAGTTA TGAAAAAATACA CAAAG	T	C	Ala	Ala	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P48200 IRON-RESPONSIVE ELEMENT BINDING PROTEIN 2 (IRE-BP 2) (IRON REGULATORY PROTEIN 2) (IRP2) - Homo sapiens (Human), 963 aa.	0.00E+00	
645	cg43277456	832	ACTTCGAGGCCT ATGTGCAGTACC G[C/T]GAGTACAT GGGCTTCATCCA GGCCA	C	T	Arg	Arg	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q02040 PROTEIN XE7 - Homo sapiens (Human), 695 aa.	0.00E+00	
646	cg43303383	232	TGGCCGAATTTC CTTCCGCTCGTG G[A/T]GCTGGGG CTGCTCCTGACC TTGGCG	A	T	Ala	Ala	SILENT-CODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:CAB45385 TRITHORAX HOMOLOGUE 2 - HOMO SAPIENS (HUMAN), 2715 aa.	0.00E+00	
647	cg43926470	2502	AGAGCCTCTTCT CCACAGCCTTCT C[C/T]GAGTCCCT GGCTGCAGAGAT CAGCT	C	T	Ser	Ser	SILENT-CODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75154 KIAA0665 PROTEIN - HOMO SAPIENS (HUMAN), 756 aa.	0.00E+00	
648	cg43971555	583	AGGTGAACTCGT GGCGCCCCGTG TC[G/A]GCAGTA GCGTCCGGGGC TTTAGGCG	G	A	Ala	Ala	SILENT-CODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAC00190 ALPHA MANNOSIDASE 6A8B - HOMO SAPIENS (HUMAN), 679 aa.	0.00E+00	

649	cg43971555	904	GGAAGCGGACA TAGGGGCAGCC AAC[G/A]TCCAGC ACAACCTCCTGG CTAAGCC	G	A	Asp	Asp	SILENT-CODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAC00190 ALPHA MANNOSIDASE 6A8B - HOMO SAPIENS (HUMAN), 679 aa.	0.00E+00	
650	cg43972478	2073	CTATGTTAGGCT GGCTTTCTATCA A[C/A]GCGTGAA GGGATGGGCAA GATGCCA	C	A	Ala	Ala	SILENT-CODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O43264 HZW10 - HOMO SAPIENS (HUMAN), 779 aa.	0.00E+00	
651	cg43986766	1862	GCACCTCCATGG TGTAGGCCGCC CC[A/G]CAGATGT CACAGCCGTACA TGGGCT	A	G	Cys	Cys	SILENT-CODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O08961 ZINC FINGER PROTEIN 104 (ROAZ) - RATTUS NORVEGICUS (RAT), 1186 aa.	0	
652	cg44932392	840	TGCTAAAGTTCA TATTTAATGAAAA [C/T]GAAGATTCT GCATCAATATCT TCCT	C	T	Ser	Ser	SILENT-CODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAD23581 CULLIN 2 - HOMO SAPIENS (HUMAN), 745 aa.	0	
653	cg43956210	1507	ATAAAGTGGAAC CTCTTGATTTTG G[C/A]GGTACTCA GAAACAGAAACA ACTTT	C	A	Gly	Gly	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P07686 BETA-HEXOSAMINIDASE BETA CHAIN PRECURSOR (EC 3.2.1.52) (N-ACETYL-BETA- GLUCOSAMINIDASE) (BETA-N-ACETYLHEXOSAMINIDASE) - Homo sapiens (Human), 556 aa.	3E-307	5 (5q13)
654	cg43982721	1732	CGTCCTGCCCAG GCAAGATCTCCG T[C/G]CCTCCTGT GCGCAACCTACA TCAGT	C	G	Val	Val	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:O14531 DIHYDROPYRIMIDINASE RELATED PROTEIN-4 (DRP-4) (ULIP4 PROTEIN) - Homo sapiens (Human), 572 aa.	1.6E-306	
655	cg43955051	494	GTTCTGACTTAA AGCAAAAATACA C[G/A]GCATAGAT TGCAACAGCAAA GAAGT	G	A	Ala	Ala	SILENT-CODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAD10823 SQUALENE EPOXIDASE (EC 1.14.99.7) - HOMO SAPIENS (HUMAN), 574 aa.	1.9E-305	8

656	cg43951838	1686	TAGCCACCGCCTTGTCCCAGACGAC[G/C]GTCATCCGCTCCTCTATCCCGTTGA	G	C	Thr	Thr	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q14194 DIHYDROPYRIMIDINASE RELATED PROTEIN-1 (DRP-1) (COLLAPSIN RESPONSE MEDIATOR PROTEIN 1) (CRMP-1) - Homo sapiens (Human), 572 aa.	3.5E-304	4 (4p16.1)
657	cg42682985	315	CTGATCCTGGCTGAAGAGGTTCCAG[C/T]GACACTTGAATAGTAACTTTTGTTT	C	T	Ser	Ser	SILENT-CODING	UNCLASSIFIED	Human Gene REMTREMBL-ACC:D1020806 (LAMBDA) DNA FOR IMMUNOGLOBLIN LIGHT CHAIN - HOMO SAPIENS (HUMAN), 541 aa (fragment).	2.00E-301	22
658	cg43917155	474	CAGTCCTTAAGAAAAGGGAGTATGG[A/C]TCAAAGTACACTCAGAATAATTTCA	A	C	Gly	Gly	SILENT-CODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAB87763 EMBRYONIC LUNG PROTEIN - HOMO SAPIENS (HUMAN), 568 aa.	2.00E-301	
659	cg43255486	1152	TCAAGCCCAACAAGCTTCGAAATGG[C/A]CACAAGGGGCTTCGGATCTTCTGCA	C	A	Gly	Gly	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:Q14451 GROWTH FACTOR RECEPTOR-BOUND PROTEIN 7 (GRB7 ADAPTER PROTEIN) (EPIDERMAL GROWTH FACTOR RECEPTOR GRB-7) (B47) - Homo sapiens (Human), 532 aa.	6.70E-294	17
660	cg43255486	1686	TCATCCTGCCGAGCGAGGAGGAGGG[C/T]CGCCTGTACTTCAGCATGGATGATG	C	T	Gly	Gly	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:Q14451 GROWTH FACTOR RECEPTOR-BOUND PROTEIN 7 (GRB7 ADAPTER PROTEIN) (EPIDERMAL GROWTH FACTOR RECEPTOR GRB-7) (B47) - Homo sapiens (Human), 532 aa.	6.70E-294	17
661	cg43926493	1341	CGCTGCTGAAGTGGACCGAGTACAC[G/A]CCAGATCCTAACCATGGCTTCTATG	G	A	Thr	Thr	SILENT-CODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAD27715 CGI-06 PROTEIN - HOMO SAPIENS (HUMAN), 574 aa.	1.40E-293	20

662	cg43316305	1345	TGTTGGGCTCCT GTTGCTCACACA A[G/A]GAGCGCC TGAGTATCCTCC GGGCAG	G	A	Lys	Lys	SILENT-CODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75708 HIRIP3 PROTEIN - HOMO SAPIENS (HUMAN), 551 aa (fragment).	8.70E-292	
663	cg42903434	103	AGGGCTGCAGC CACGGTCTCCAG AT[A/G]TTGCCCA GCCTGTCCAGCT GCAGAG	A	G	Asn	Asn	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P51690 ARYLSULFATASE E PRECURSOR (EC 3.1.6.-) (ASE) - Homo sapiens (Human), 589 aa.	2.30E-291	
664	cg42903434	67	CCCTAAGGCACC AGCAGAGGGGG AA[C/T]GGGCCA CAGCAGGGCTG CAGCCACG	C	T	Pro	Pro	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P51690 ARYLSULFATASE E PRECURSOR (EC 3.1.6.-) (ASE) - Homo sapiens (Human), 589 aa.	2.3E-291	
665	cg43949262	837	GCTGCTCTCTCA CCACTGCAAGCT C[C/T]GCGTCCCC ACGCAGTGTCAC TGAGCA	C	T	Ala	Ala	SILENT-CODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:BAA76832 KIAA0988 PROTEIN - HOMO SAPIENS (HUMAN), 1192 aa.	9E-290	
666	cg43995003	1790	TTTGTGGAATGA CATCAAATGGTT T[C/T]ACCATTGC AGACCCAGATGA TAGAG	C	T	Phe	Phe	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P10155 60 KD RO PROTEIN (60 KD RIBONUCLEOPROTEIN RO) (RORNP) (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) - Homo sapiens (Human), 538 aa.	1.9E-289	1
667	cg43926814	645	AACCAAAAGGAT CTTCCTCAAACT G[A/C]ACTGGTC CTTCTCGGCCTC TCTGTC	A	C	Val	Val	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:Q13573 NUCLEAR PROTEIN SKIP (SNW1 PROTEIN) (NUCLEAR RECEPTOR COACTIVATOR NCOA-62) - Homo sapiens (Human), 536 aa.	5E-289	14
668	cg44028870	446	AGAAAATAAAAA TGTCGACCTCGT C[C/T]TTGAGGC GCCAGATGAAGA ACATCG	C	T	Ser	Ser	SILENT-CODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:BAA83017 KIAA1065 PROTEIN - HOMO SAPIENS (HUMAN), 641 aa.	5.6E-288	

669	cg40918088	1907	CAAAAGCCACAGAGGGCCGGATCAT[T/A]ACAGTGGAGGATCACTACCCGCAAG	T	A	Ile	Ile	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P51854 TRANSKETOLASE 2 (EC 2.2.1.1) (TK 2) (TRANSKETOLASE RELATED PROTEIN) - Homo sapiens (Human), 557 aa.	1.8E-287	X (Xq28)
670	cg43129343	1526	TGGTCGAAGGTCAGGGCGAGAAGAA[C/T]GTGACCTTCTGGGGGAGACCGCTGC	C	T	Asn	Asn	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P27918 PROPERDIN PRECURSOR - Homo sapiens (Human), 469 aa.	2.2E-286	X (Xp11.4)
671	cg43931056	1275	TGGCCATGGAGAGACATGGACTTGA[T/C]CATCAAGTAATTTCTGTAACCTTCG	T	C	Asp	Asp	SILENT-CODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q15020 ORF - HOMO SAPIENS (HUMAN), 963 aa.	4.5E-286	12
672	cg43968641	3598	CGATGGCCAGGCCATCGATGAAATT[A/G]TGGAGGCCGTCGCTCAGAGTGATCA	A	G	His	His	SILENT-CODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q15043 MRNA (KIAA0062) FOR ORF (NOVEL PROTEIN), PARTIAL CDS - HOMO SAPIENS (HUMAN), 531 aa (fragment).	2E-285	8
673	cg43949830	1018	TTGAGATGTAGCACTCACATGCTTT[G/A]TTTCCTAAATAATTTATAACCTCAG	G	A	Asn	Asn	SILENT-CODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q92617 MYELOBLAST KIAA0220 - HOMO SAPIENS (HUMAN), 553 aa (fragment).	2.7E-281	16
674	cg43949830	793	TTTTCATGTCTATTTTTTCTTTTGA[T/C]CCTCCAGCAAGTAGATTGATATTTT	T	C	Gly	Gly	SILENT-CODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q92617 MYELOBLAST KIAA0220 - HOMO SAPIENS (HUMAN), 553 aa (fragment).	2.7E-281	16

675	cg44002920	1169	TCTGCAGCAGCA GTGAATCAGATA C[A/G]TTGGGATT TTTCAAATACTG GCACA	A	G	Asn	Asn	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P42785 LYSOSOMAL PRO-X CARBOXYPEPTIDASE PRECURSOR (EC 3.4.16.2) (PROLYLCARBOXYPEPTIDASE) (PRCP) (PROLINE CARBOXYPEPTIDASE) (ANGIOTENSINASE C) (LYSOSOMAL CARBOXYPEPTIDASE C) - Homo sapiens (Human), 496 aa.	6.7E-278	11
676	cg44002920	644	CAAAGTTTCTC AGTGCTGCTTTC C[C/T]GCACTGTC ATAGAAATCTCT GATCC	C	T	Ala	Ala	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P42785 LYSOSOMAL PRO-X CARBOXYPEPTIDASE PRECURSOR (EC 3.4.16.2) (PROLYLCARBOXYPEPTIDASE) (PRCP) (PROLINE CARBOXYPEPTIDASE) (ANGIOTENSINASE C) (LYSOSOMAL CARBOXYPEPTIDASE C) - Homo sapiens (Human), 496 aa.	6.7E-278	11
677	cg43922691	1088	TGGCTGGAAAGT TAATTCCTGTGC A[C/T]CAAGTGAG AGGTTTGAAAGA GAAGA	C	T	His	His	SILENT-CODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAD34043 CGI-48 PROTEIN - HOMO SAPIENS (HUMAN), 521 aa.	8.5E-278	17
678	cg43922691	416	ACGAGGACGCG TTGCTGCGGCGT CT[G/A]CGAGGC CCGAGGGTTCAA GAACATG	G	A	Leu	Leu	SILENT-CODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAD34043 CGI-48 PROTEIN - HOMO SAPIENS (HUMAN), 521 aa.	8.5E-278	17
679	cg43922691	788	CCACATCAACTT CTCTTCCAAGAG G[C/A]ATCTTGAA GATGAAGAACTG CCAGC	C	A	Gly	Gly	SILENT-CODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAD34043 CGI-48 PROTEIN - HOMO SAPIENS (HUMAN), 521 aa.	8.50E-278	17

680	cg43984386	374	CGCGGAGGGTC ACCAACGTGGG GTC[T/C]CTGTTG CTCACCCCGCAG GAGAACG	T	C	Ser	Ser	SILENT-CODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O00401 N-WASP - HOMO SAPIENS (HUMAN), 505 aa.	5.90E-277	
681	cg42935995	1294	CAATCTTCTGGC TCAGGTAGATTA G[C/T]TCCTCTGT CCGTCGCATACT CTGGA	C	T	Glu	Glu	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:Q12774 PROBABLE GUANINE NUCLEOTIDE REGULATORY PROTEIN TIM (ONCOGENE TIM) (P60 TIM) (TRANSFORMING IMMORTALIZED MAMMARY ONCOGENE) - Homo sapiens (Human), 519 aa.	1.00E-274	
682	cg43929467	717	AAAACTTGGTGG AGTTCACAGATG A[A/G]GAGGGAT ATGGTCGTTATC TCGATC	A	G	Glu	Glu	SILENT-CODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q12874 SPLICESOME-ASSOCIATED PROTEIN SAP 61 - HOMO SAPIENS (HUMAN), 501 aa.	1.30E-274	1
683	cg43947753	641	TCCCCGAGCGT GTAGGAGCAGT GCG[A/G]TCGTG GTCCCTCCCTAT GCAGCCTG	A	G	Arg	Arg	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q13610 PERIODIC TRYPTOPHAN PROTEIN 1 HOMOLOG (KERATINOCYTE PROTEIN IEF SSP 9502) - Homo sapiens (Human), 501 aa.	7.10E-274	12
684	cg43333012	1838	TGTTCATGAGCT TTGGAAAAGCTG C[T/C]AATAAGCC CTCAATCCGAGT TCGGG	T	C	Leu	Leu	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P48444 COATOMER DELTA SUBUNIT (DELTA-COAT PROTEIN) (DELTA-COP) (ARCHAIN) - Homo sapiens (Human), 511 aa.	3.50E-272	11 (11q23.3)
685	cg43333012	1861	GCTAATAAGCCC TCAATCCGAGTT C[G/T]GGTCATTT CCACAAACTGTC GAGAA	G	T	Arg	Arg	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P48444 COATOMER DELTA SUBUNIT (DELTA-COAT PROTEIN) (DELTA-COP) (ARCHAIN) - Homo sapiens (Human), 511 aa.	3.50E-272	11 (11q23.3)
686	cg43333012	407	CAGCTCCCTCTT CTTGGTATTACA A[A/G]ATTTCATA CTTATCCACTAG GAAAG	A	G	Ile	Ile	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P48444 COATOMER DELTA SUBUNIT (DELTA-COAT PROTEIN) (DELTA-COP) (ARCHAIN) - Homo sapiens (Human), 511 aa.	3.50E-272	11 (11q23.3)

687	cg43926574	972	AAGATCTAAGAC ATTTAATAGTATC [A/G]AGAAGTACA CAGGCACCACTA ATAA	A	G	Ser	Ser	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P43490 PRE-B CELL ENHANCING FACTOR PRECURSOR - Homo sapiens (Human), 491 aa.	1.10E-268	7
688	cg42869211	1895	TGCACTGAAAAG CTTGATTCCTAC A[T/C]TGGAAAAA ACCAAAAGCACC AGCAA	T	C	Leu	Leu	SILENT-CODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q15397 ORF, COMPLETE CDS - HOMO SAPIENS (HUMAN), 508 aa.	7.00E-267	9
689	cg43031103	1702	CCCTCCCCTTGG TTGAGGAGACAG C[A/G]GGGGCTG GTGTGAGGTGCA GCACCC	A	G	Pro	Pro	SILENT-CODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O60240 PERILIPIN - HOMO SAPIENS (HUMAN), 522 aa.	6.30E-266	
690	cg43313186	495	TCTCATTTCCAA GATCTTCAAGGG A[T/C]TGGCAGCT GACCAGACAGA GGCCCT	T	C	Leu	Leu	SILENT-CODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q16438 ALPHA 1 SYNTROPHIN - HOMO SAPIENS (HUMAN), 505 aa.	8.30E-265	20 (20q11.2)
691	cg43922182	1285	CTTCCCGCGGG AGCCGCGGCCC AAG[T/C]TGCACC ACAGCCTCAGCT TCTCGGG	T	C	Leu	Leu	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P47974 TIS11D PROTEIN (BUTYRATE RESPONSE FACTOR 2) (EGF-RESPONSE FACTOR 2) (ERF-2) - Homo sapiens (Human), 482 aa.	1.10E-261	2
692	cg43922182	1476	CCTCCGCGGCC TCCACGCCCTCG GG[C/G]GCCCCG ACATGCTGCGCC TCCGCGG	C	G	Gly	Gly	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P47974 TIS11D PROTEIN (BUTYRATE RESPONSE FACTOR 2) (EGF-RESPONSE FACTOR 2) (ERF-2) - Homo sapiens (Human), 482 aa.	1.10E-261	2
693	cg27359628	196	GAGACAGCGTG CCACACAACCAC CC[T/C]ACCAAGT TCAAGGTGACAA ATGTGG	T	C	Pro	Pro	SILENT-CODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O43559 FGFR SIGNALLING ADAPTOR SNT-2 - HOMO SAPIENS (HUMAN), 492 aa.	2.30E-260	

694	cg43980777	999	ATAATTTTCTGAAATCCATGGGCTC[T/A]GGTACAATCTGGGGTCGTGAGCAAG	T	A	Pro	Pro	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P23497 NUCLEAR AUTOANTIGEN SP-100 (SPECKLED 100 KD) - Homo sapiens (Human), 688 aa.	6.20E-259	2
695	cg43980777	882	CATGCTTGCTTCTCAGTGCCCCGCT[C/T]GAGGCTTCTGCGGGCGCCTCCTCCT	C	T	Ser	Ser	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P23497 NUCLEAR AUTOANTIGEN SP-100 (SPECKLED 100 KD) - Homo sapiens (Human), 688 aa.	6.20E-259	2
696	cg43986498	1090	CGGAGGAGGAGCTGGAGCGGCTGGA[G/A]GAGGCCTGCGACATGGCGCTGGAGC	G	A	Glu	Glu	SILENT-CODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:CAB43677 HYPOTHETICAL 55.4 KD PROTEIN - HOMO SAPIENS (HUMAN), 499 aa.	1.30E-255	19
697	cg43986498	1664	CCGGAAGCAGGCCAACCGTATGAGC[A/T]NCGGAGAGATCGAGGAGGACGCCTA	A	T	???	???	SILENT-CODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:CAB43677 HYPOTHETICAL 55.4 KD PROTEIN - HOMO SAPIENS (HUMAN), 499 aa.	1.30E-255	19
698	cg39711096	941	ACGTGGAGGTGGACATGTCGGGAGA[C/T]TTGGGGTGGCTGTTGAACCTCTTCC	C	T	Asp	Asp	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P18428 LIPOPOLYSACCHARIDE-BINDING PROTEIN PRECURSOR (LBP) - Homo sapiens (Human), 481 aa.	1.00E-251	
699	cg39711096	953	ACATGTCGGGAGACTTGGGGTGGCT[G/C]TTGAACCTCTTCCACAACCAGATTG	G	C	Leu	Leu	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P18428 LIPOPOLYSACCHARIDE-BINDING PROTEIN PRECURSOR (LBP) - Homo sapiens (Human), 481 aa.	1.00E-251	
700	cg42101957	279	TTTATGTAAATAATGGGTTTCGGTC[G/A]TTGTTAAGATGTTGTGCCAAATGAC	G	A	Asn	Asn	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P04279 SEMENOGELIN I PROTEIN PRECURSOR (SGI) [CONTAINS: SEMINAL BASIC PROTEIN; ALPHA-INHIBIN-92; ALPHA-INHIBIN-31] - Homo sapiens (Human), 462 aa.	5.50E-251	20 (20q12)

701	cg44910581	1321	CAACTGCCTGTC CAAGTGTTGCGC C[G/A]CAACACTT GGACCTCGTCCT AGTTT	G	A	Pro	Pro	SILENT-CODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q16349 H-NUC - HOMO SAPIENS (HUMAN), 824 aa.	5.80E-251	
702	cg44910581	2649	AACTGGACAAAG CATTAGCTTGTT T[T/C]CGAAATGC TATCAGGGTCAA TCCTA	T	C	Phe	Phe	SILENT-CODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q16349 H-NUC - HOMO SAPIENS (HUMAN), 824 aa.	5.80E-251	
703	cg43950250	675	GTTCCTCTACTT CGGGTGGGAAG TC[G/A]GGGTTCT GGAATTGCTGCA TGAGTT	G	A	Pro	Pro	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P11926 ORNITHINE DECARBOXYLASE (EC 4.1.1.17) (ODC) - Homo sapiens (Human), 461 aa.	7.00E-251	2 (2p25)
704	cg43962278	371	AGAGGGTGAGG GTCTGGAGGACT CC[T/A]GTGGTG CAGGCCATCTCC CGGATAG	T	A	Thr	Thr	SILENT-CODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAD01211 ASPARTYL AMINOPEPTIDASE - HOMO SAPIENS (HUMAN), 472 aa.	1.50E-250	2
705	cg44027341	957	GCACTGGTTTCC GCCTCCGACCTG T[A/G]GCTGGCC TGCTTTCCTCTC GGGATT	A	G	Val	Val	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P00439 PHENYLALANINE-4-HYDROXYLASE (EC 1.14.16.1) (PAH) (PHE-4-MONOOXYGENASE) - Homo sapiens (Human), 452 aa.	1.60E-246	12
706	cg43996564	739	AGAGGGCACCC CGCAGGCTCAG GGG[C/G]CCACC ACCAGGCGTGA GCTGGATGG	C	G	Gly	Gly	SILENT-CODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q12794 TUMOR SUPPRESSOR (LUCA-1) - HOMO SAPIENS (HUMAN), 435 aa.	2.90E-245	3
707	cg43980318	600	GCCCAGTTTATT CGTCCAAAGCTG C[A/T]GGGAGTG GACTCAGGATGT GCGACC	A	T	Ala	Ala	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P30520 ADENYLOSUCCINATE SYNTHETASE (EC 6.3.4.4) (IMP--ASPARTATE LIGASE) - Homo sapiens (Human), 455 aa.	1.60E-244	1 (1cen)

708	cg43985156	1497	CTCTCAAGTTCA TGCTGACGAATC T[T/G]AAGTGGG GTCTTGCTTGGG TGTCCT	T	G	Leu	Leu	SILENT-CODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75595 BCL-2-INTERACTING PROTEIN BECLIN - HOMO SAPIENS (HUMAN), 450 aa.	1.80E-243	17
709	cg42897932	675	ATTATATCTCTG GGATCCAGACTA T[T/C]GGACATAG GGTAATTGTATC TGATG	T	C	Ile	Ile	SILENT-CODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:BAA32662 KIAA0017 PROTEIN - HOMO SAPIENS (HUMAN), 1217 aa.	8.20E-241	16
710	cg43936335	747	AAAGGGAAATGA GGAGGAGTAGT GG[A/T]TTGCGA GCAGGTTCTCGG AGGGACC	A	T	Gly	Gly	SILENT-CODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:BAA74919 KIAA0896 PROTEIN - HOMO SAPIENS (HUMAN), 1230 aa (fragment).	8.50E-239	8
711	cg44013460	1019	TCACTGAGTTGA AAAAGCTGGACT T[C/G]CCAGCTC CAATTGGACCCA GCAGCA	C	G	Gly	Gly	SILENT-CODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q14496 HEPATITIS C-ASSOCIATED MICROTUBULAR AGGREGATE PROTEIN P44 - HOMO SAPIENS (HUMAN), 444 aa.	2.60E-237	1
712	cg44013460	1040	ACTTCCCAGCTC CAATTGGACCCA G[C/G]AGCAGAA TTCGTATTTGTT GAACCA	C	G	Leu	Leu	SILENT-CODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q14496 HEPATITIS C-ASSOCIATED MICROTUBULAR AGGREGATE PROTEIN P44 - HOMO SAPIENS (HUMAN), 444 aa.	2.60E-237	1
713	cg44013460	1043	TCCCAGCTCCAA TTGGACCCAGCA G[C/G]AGAATTC GTATTTGTTGAA CCAGGG	C	G	Leu	Leu	SILENT-CODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q14496 HEPATITIS C-ASSOCIATED MICROTUBULAR AGGREGATE PROTEIN P44 - HOMO SAPIENS (HUMAN), 444 aa.	2.60E-237	1
714	cg43948360	2144	CCACACCTGTCA GATCGGGCGAG CT[G/C]CGGAAC GCGTCAGCCCA GGACTGGA	G	C	Arg	Arg	SILENT-CODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O88746 TOM1 - MUS MUSCULUS (MOUSE), 492 aa.	5.10E-234	22

715	cg43962127	363	CCAAGAAGAAGATGTTGTTGAACTG[C/T]GTTGCACAAAGTTTCTTGACCTCTT	C	T	Thr	Thr	SILENT-CODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAD34038 CGI-43 PROTEIN - HOMO SAPIENS (HUMAN), 483 aa.	1.10E-233	7
716	cg43962127	678	TAAACTGGGGTTCTTTCTCAGACCC[G/A]GACATCCTCTTGTTGATGTTAAACT	G	A	Ser	Ser	SILENT-CODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAD34038 CGI-43 PROTEIN - HOMO SAPIENS (HUMAN), 483 aa.	1.10E-233	7
717	cg43940463	1031	AGAAATGGCTGCAGCGCTGGAACTC[A/G]GGCCCTCCTCCGCTCAGACTCAGCT	A	G	Pro	Pro	SILENT-CODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q99771 JIP-1 - HOMO SAPIENS (HUMAN), 467 aa.	3.10E-232	
718	cg43933074	206	CCGACCTCAACCGCAAGGACAAGTT[T/C]CCCGCCATCACCCACCTCAAGTTCC	T	C	Phe	Phe	SILENT-CODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAD31087 VITAMIN D RECEPTOR INTERACTING PROTEIN - HOMO SAPIENS (HUMAN), 873 aa.	3.20E-228	19
719	cg43984330	868	CGAGACCCCGCTTCTCCCGGTTGTC[A/G]CTGAGCAGTGGGGTTATGGTGTACA	A	G	Ser	Ser	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P32121 BETA-ARRESTIN 2 - Homo sapiens (Human), 409 aa.	8.50E-223	17
720	cg43999712	467	CCCTGGCAGTGGCCGCTGTGCTATA[C/T]CACAAGATGAACAGCGGGAAGCAGG	C	T	Tyr	Tyr	SILENT-CODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O43813 SEVENTRANSMEMBRANE-DOMAIN PROTEIN - HOMO SAPIENS (HUMAN), 399 aa.	3.30E-221	2
721	cg43994204	1151	GCATCGCCACATCCCTGGATGGCTT[C/T]GACGTCGCGTCCGTGCAGCAGCAGC	C	T	Phe	Phe	SILENT-CODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O60664 CARGO SELECTION PROTEIN TIP47 - HOMO SAPIENS (HUMAN), 434 aa.	5.40E-221	19

722	cg43994204	1157	CCACATCCCTGG ATGGCTTCGACG T[C/T]GCGTCCGT GCAGCAGCAGC GGCAGG	C	T	Val	Val	SILENT-CODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O60664 CARGO SELECTION PROTEIN TIP47 - HOMO SAPIENS (HUMAN), 434 aa.	5.40E-221	19
723	cg43960557	1813	TGAAATCAAGGG CCTGGTAGACGA G[T/C]GAGTAGA GGTATTCCACCT TCTTAC	T	C	Ser	Ser	SILENT-CODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q13391 HYPOTHETICAL PROTEIN 384D8_6 - HOMO SAPIENS (HUMAN), 533 aa.	2.70E-220	22
724	cg43251548	1238	ATAGTCAGGTTG ATTGGACTTACG A[T/C]CCAAATGA ACCTCGATACTG CATTT	T	C	Asp	Asp	SILENT-CODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O60394 PAC CLONE DJ0872F07 FROM 7Q31, COMPLETE SEQUENCE - HOMO SAPIENS (HUMAN), 408 aa (fragment).	2.70E-217	
725	cg43068795	633	CTCCTTCTTTCT CCTTCCTCTGTT C[C/T]CGTTCCTC TTTCATATCTCTA AGTA	C	T	Arg	Arg	SILENT-CODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:CAB51071 HYPOTHETICAL 295.8 KD PROTEIN - HOMO SAPIENS (HUMAN), 2701 aa.	2.80E-215	1
726	cg43990581	767	ACCCGTACCTCC CGCTCGTCACCG A[T/C]GAGGACA GCTGGTACAGCA AGTGGC	T	C	Asp	Asp	SILENT-CODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O60651 RAP2 INTERACTING PROTEIN 8 - HOMO SAPIENS (HUMAN), 405 aa.	1.60E-214	17
727	cg43083763	776	CCCTGAACGCCC CTCCAGGGACCT C[A/G]CTCATCTC CTTCAGTGACAA GGCCA	A	G	Ser	Ser	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P21549 SERINE--PYRUVATE AMINOTRANSFERASE (EC 2.6.1.51) (SPT) (ALANINE-- GLYOXYLATE AMINOTRANSFERASE) (EC 2.6.1.44) (AGT) - Homo sapiens (Human), 392 aa.	1.10E-211	2 (2q36)
728	cg43984681	666	ACCCAGCCTTCA TCCGGGCCTGG G[T/G]GGCGGG GTCGGCAACTAC AAGTTAG	G	T	Val	Val	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:O15382 BRANCHED-CHAIN AMINO ACID AMINOTRANSFERASE, MITOCHONDRIAL PRECURSOR (EC 2.6.1.42) (BCAT(M)) - Homo sapiens (Human), 392 aa.	1.30E-210	19 (19q13)

729	cg44927668	1463	ATCAGGCTGCGTTTTTGAGTCAAGC[C/T]TCACAGATGTACGACTCCTCTTTGA	C	T	Ala	Ala	SILENT-CODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:CAB48885 DJ462O23.2 (NOVEL PROTEIN) - HOMO SAPIENS (HUMAN), 406 aa.	2.10E-210	1
730	cg43948416	2020	TTTTAGGACGACCCCGTAAGAAATT[T/C]TGCATGCTATTAAGTGCATCCATAG	T	C	Gln	Gln	SILENT-CODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAD44976 PROTEIN PHOSPHATASE METHYLESTERASE-1 - HOMO SAPIENS (HUMAN), 386 aa.	4.70E-206	11
731	cg43959472	1584	TCTTGAGCCACACGATGCCGCAGGT[A/G]CGCGTGAAGGGGTTCTCGTTGATCT	A	G	Arg	Arg	SILENT-CODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O14498 ISLR PRECURSOR - HOMO SAPIENS (HUMAN), 428 aa.	2.40E-203	15
732	cg43921081	528	ACAAGAGAAGAGAATTTATCACCGG[T/C]GATGTTGAACCAACAGATGCGGAAT	T	C	Gly	Gly	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q99733 NUCLEOSOME ASSEMBLY PROTEIN 1-LIKE 4 (NUCLEOSOME ASSEMBLY PROTEIN 2) (NAP2) - Homo sapiens (Human), 375 aa.	3.10E-202	11
733	cg44128902	965	AGATGGAGTCAGCAGATCAGGCCGT[T/C]GCTGAGCTCAACGGGACCCAGGTGG	T	C	Val	Val	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P18615 RD PROTEIN - Homo sapiens (Human), 380 aa.	1.00E-201	1 (1p36.2)
734	cg44128902	761	GGGATCGAGACCGAGACCGAGAGGG[T/G]CCTTTCCGCAGGTCGGATTCATTCC	T	G	Gly	Gly	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P18615 RD PROTEIN - Homo sapiens (Human), 380 aa.	1.00E-201	1 (1p36.2)
735	cg44128902	797	GGTCGGATTCATTCCCTGAACGGCG[A/T]GCCCCTAGGAAAGGGAATACTCTCT	A	T	Arg	Arg	SILENT-CODING	UNCLASSIFIED	Human Gene S[illegible]OT-ACC:P18615 RD PROTEIN - Homo sapiens (Human), 380 aa.	1.00E-201	1 (1p36.2)

736	cg43289239	822	TCACCACCCTGCCCCATGTGCAGAA[A/G]TACCTGAAGTCCGTACGCTACATTG	A	G	Lys	Lys	SILENT-CODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O15059 KIAA0351 - HOMO SAPIENS (HUMAN), 557 aa.	1.50E-199	9
737	cg43320965	1607	GTGATACAAGGCAGAGCCTGCAGCA[A/G]TCCATGCCTCCCTGTGAGCCACCAT	A	G	Gln	Gln	SILENT-CODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAD30184 HYPOTHETICAL 43.8 KD PROTEIN - HOMO SAPIENS (HUMAN), 391 aa.	5.30E-198	14
738	cg43944615	2020	CATAGCTGTAGTTTTTGCTGAGATA[C/T]GTTGCCAAAGTTGGCTTCACCTTTT	C	T	Thr	Thr	SILENT-CODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O14877 FRPHE - HOMO SAPIENS (HUMAN), 346 aa.	1.30E-192	
739	cg43935935	777	TCCAGTCAGAAATCCATTTTCTAAC[T/C]TGATCCAGCTCAGTTGGGATGTACT	T	C	Gln	Gln	SILENT-CODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O60735 GA17 PROTEIN - HOMO SAPIENS (HUMAN), 374 aa.	1.70E-192	X
740	cg43964795	2166	CCACGAGGTAGTCTTCCCGGATAAT[G/A]TGCTCCACACGGATCCGAGCTCGTT	G	A	His	His	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P53990 HYPOTHETICAL PROTEIN KIAA0174 - Homo sapiens (Human), 364 aa.	5.80E-192	16
741	cg43980381	460	ACACCCTCAGGACCAAGAAGAACAC[T/A]GCCATTGTCAAGCGCTGGAGCGACC	T	A	Thr	Thr	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:Q03385 GUANINE NUCLEOTIDE DISSOCIATION STIMULATOR RALGDS FORM A (RALGEF) - Mus musculus (Mouse), 852 aa.	5.60E-191	9
742	cg43996402	1312	GTGCAAACCCACTGTTTCTCATCTC[C/G]GCTATTAGCTCCGAGGGGTGCATCG	C	G	Ala	Ala	SILENT-CODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q12804 RECEPIN - HOMO SAPIENS (HUMAN), 451 aa.	2.60E-189	2

743	cg43933608	390	CCTTGAGTTTCA GGAGGGGCTGT AA[G/A]GTGAAGA AGCATGAAACTC AGTCTC	G	A	Lys	Lys	SILENT-CODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75410 TACC1 - HOMO SAPIENS (HUMAN), 805 aa.	4.50E-189	8
744	cg43249389	924	GCTTCAACCGGT CCCGGGAGTATC A[G/A]CTCAACGA CTCTGCCAAATA CTACC	G	A	Gln	Gln	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P09471 GUANINE NUCLEOTIDE-BINDING PROTEIN G(O), ALPHA SUBUNIT 1 - Homo sapiens (Human), 353 aa.	1.40E-188	15
745	cg43947129	1282	TTCTATTTTGGG GCTCCACTGGAC A[A/C]ACGTAGAA TCCTTGAGAATT ATCAA	A	C	Val	Val	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P10658 PROBABLE PHOSPHOSERINE AMINOTRANSFERASE (EC 2.6.1.52) (PSAT) (ENDOMETRIAL PROGESTERONE-INDUCED PROTEIN) (EPIP) - Oryctolagus cuniculus (Rabbit), 370 aa.	3.00E-188	
746	cg43927276	1007	CAGCCTATGGAG GCCTCAATGAGA A[A/G]TCTTTTGT AGATGGCTTGAA TTTTA	A	G	Lys	Lys	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P50616 TOB PROTEIN (TRANSDUCER OF ERBB-2) - Homo sapiens (Human), 345 aa.	3.10E-186	17
747	cg43957632	893	TGCCTCCCCCGC CCAACATGTTCA T[G/A]GTGCTGTC CACGTGGTTCTC CACCA	G	A	Thr	Thr	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P18065 INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 2 PRECURSOR (IGFBP-2) (IBP-2) (IGF-BINDING PROTEIN 2) - Homo sapiens (Human), 328 aa.	2.2E-185	2 (2q33)
748	cg43957632	1061	GCTCGGAGCCC GGGTGGGGATA GCA[G/C]CGCAG CCCCTGGCCGC AGCGCGGGG	G	C	Arg	Arg	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P18065 INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 2 PRECURSOR (IGFBP-2) (IBP-2) (IGF-BINDING PROTEIN 2) - Homo sapiens (Human), 328 aa.	2.2E-185	2 (2q33)

749	cg43950796	369	AGTAGTACCGCT GCCAGCCCTGTC G[T/C]GTCCGCT CTTCCTCAGGAG CAGGGA	T	C	Thr	Thr	SILENT-CODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:CAB45684 C14ORF3 PROTEIN - HOMO SAPIENS (HUMAN), 338 aa.	2.5E-184	
750	cg44001387	770	GCTGTCTGGTTG TGCTCCCAGGCA C[A/G]CACAAGG GCTCCCTGAAGC CCCACG	A	G	Thr	Thr	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:O14832 PEROXISOMAL PHYTANOYL-COA ALPHA-HYDROXYLASE PRECURSOR (PHYTANIC ACID OXIDASE) - Homo sapiens (Human), 338 aa.	8.4E-184	10
751	cg43917229	245	GCCCACTTGCAA CCAGGAGAGCAT T[C/T]CTAAAGAA GAAAGGGCTGA CAGATG	C	T	Phe	Phe	SILENT-CODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75381 PEROXISOMAL MEMBRANE ANCHOR PROTEIN HSPEX14P - HOMO SAPIENS (HUMAN), 377 aa.	1.6E-180	1
752	cg43981031	525	CTGCTATCCCTT TATGAGAGGGAG A[C/T]AAGGTCTG AAGTTTGTTTCC CAAAG	C	T	Leu	Leu	SILENT-CODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAD34057 CGI-62 PROTEIN - HOMO SAPIENS (HUMAN), 325 aa.	1E-178	
753	cg43919917	1068	ATGACTCAGAGC AGGTGCCCCAG GC[A/C]CTCCGC CGGCTCCGCCC GCGCACCC	A	C	Ala	Ala	SILENT-CODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O60808 BK833B7.1 - HOMO SAPIENS (HUMAN), 339 aa.	3.5E-178	22
754	cg43989723	426	AGCTGCGGGGC CGGAGCGAGGC TGA[G/A]ATCCG GGTCTTCCTCCA GCAGCTCA	G	A	Glu	Glu	SILENT-CODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q13486 PSE-BINDING FACTOR PTF DELTA SUBUNIT - HOMO SAPIENS (HUMAN), 334 aa.	1.5E-175	
755	cg43931789	116	CGGCAGCGTCG CTGGAGCTGTG GCT[G/C]AACAAA GCCACAGACCCA AGCATGT	G	C	Leu	Leu	SILENT-CODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O14564 HYPOTHETICAL 67.1 KD PROTEIN - HOMO SAPIENS (HUMAN), 613 aa.	2E-175	16

756	cg43967532	3684	TCATGGCGATGCAGACGTCCCCCTC[G/C]GGGAACTTGTCACACTTAAGCATCT	G	C	Pro	Pro	SILENT-CODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O14779 SECRETED APOPTOSIS RELATED PROTEIN 2 - HOMO SAPIENS (HUMAN), 314 aa.	2.30E-174	8
757	cg43967532	3843	AGAGCGAGCAGAGGAAGACCTGGGT[G/C]CCGGCGTGGCAGTTCTTGTTGAGCA	G	C	Gly	Gly	SILENT-CODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O14779 SECRETED APOPTOSIS RELATED PROTEIN 2 - HOMO SAPIENS (HUMAN), 314 aa.	2.30E-174	8
758	cg43250735	1560	TGATGATGTGGCTCTGGAACTTGTT[G/A]AAGTAGATAGAACCGTTGTAGACCA	G	A	Phe	Phe	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:Q62609 NEURONAL OLFACTOMEDIN-RELATED ER LOCALIZED PROTEIN PRECURSOR (NOEL) (1B426B) - *Rattus norvegicus* (Rat), 485 aa.	1.20E-173	9
759	cg43918085	877	CACCCATGGGACCATCTGACCCAGG[A/G]CCCATTGGAAAATTAGGTCTGTTAG	A	G	Gly	Gly	SILENT-CODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:CAB45699 HYPOTHETICAL 37.9 KD PROTEIN - HOMO SAPIENS (HUMAN), 361 aa.	1.90E-173	
760	cg43927536	1855	GAGCTGGTGTGGTAACTCTGGTTAC[A/G]AATTTGGAAGAACTGGCATATGCAG	A	G	Phe	Phe	SILENT-CODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O60667 ANTI-FAS-INDUCED APOPTOSIS - HOMO SAPIENS (HUMAN), 390 aa.	3.80E-172	
761	cg43923012	1198	CTAACTCTACCACCTGCATTCCCACC[A/G]TAAAGACTGTACATGTCATCTGCAA	A	G	Tyr	Tyr	SILENT-CODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:CAB43210 HYPOTHETICAL 37.0 KD PROTEIN - HOMO SAPIENS (HUMAN), 330 aa (fragment).	9.10E-171	X
762	cg43941339	1200	TGGAGTCCTGGCTGTCCACATGGTC[A/G]TCATCATCTTCATCATCCATATCAT	A	G	Asp	Asp	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P10451 OSTEOPONTIN PRECURSOR (BONE SIALOPROTEIN 1) (URINARY STONE PROTEIN) (SECRETED PHOSPHOPROTEIN 1) (SPP-1) (NEPHROPONTIN) (UROPONTIN) - Homo sapiens (Human), 314 aa.	8.20E-170	4 (4q21)

763	cg43251632	646	TAAGTTGTTTGT GTGTCACTGTGA C[G/A]GCTCCCA CGGTTGTTTCCT TTGGCA	G	A	Ala	Ala	SILENT-CODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAD38537 TRANSPORTIN-SR - HOMO SAPIENS (HUMAN), 975 aa.	2.50E-169	
764	cg44032718	435	GGGAGGCACCT GCCACCCAGGC CTC[G/A]TCTACT ACTCAGCTGACT GATACCC	G	A	Ser	Ser	SILENT-CODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O76058 DJ14O9.2 (MELANOMA-ASSOCIATED ANTIGEN MAGE LIKE) - HOMO SAPIENS (HUMAN), 606 aa.	5.70E-169	X
765	cg44032718	807	CAGGTGGCCGA AGGGTCTCAAAG GC[T/C]CTAATGG CCTCAATGGCCC GCAGGG	T	C	Ala	Ala	SILENT-CODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O76058 DJ14O9.2 (MELANOMA-ASSOCIATED ANTIGEN MAGE LIKE) - HOMO SAPIENS (HUMAN), 606 aa.	5.70E-169	X
766	cg43959938	1549	TGCATCCAGCAC ACTTCTTGGCCA C[A/G]AAGTTCTT GTAGCAATCCAC GCAGT	A	G	Phe	Phe	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:Q13642 SKELETAL MUSCLE LIM-PROTEIN 1 (SLIM 1) (SLIM) (FOUR AND A HALF LIM DOMAINS PROTEIN 1) (FHL-1) - Homo sapiens (Human), 280 aa.	5.20E-168	X
767	cg43329903	874	TCCGGATCCTCC CAGCCCAGAGC CG[A/G]GCCCTC GGAGGCCCTCC AGAATACC	A	G	Arg	Arg	SILENT-CODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q16664 PROTEIN A-1 - HOMO SAPIENS (HUMAN), 304 aa.	5.90E-167	12
768	cg43329903	883	TCCCAGCCCAGA GCCGAGCCCTC GG[A/G]GGCCCT CCAGAATACCTG GGACAAA	A	G	Gly	Gly	SILENT-CODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q16664 PROTEIN A-1 - HOMO SAPIENS (HUMAN), 304 aa.	5.90E-167	12
769	cg43329903	892	AGAGCCGAGCC CTCGGAGGCCC TCC[A/T]GAATAC CTGGGACAAAGA CACAGGC	A	T	Pro	Pro	SILENT-CODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q16664 PROTEIN A-1 - HOMO SAPIENS (HUMAN), 304 aa.	5.90E-167	12

770	cg43329903	895	GCCGAGCCCTC GGAGGCCCTCC AGA[A/G]TACCTG GGACAAAGACAC AGGCTGG	A	G	Glu	Glu	SILENT-CODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q16664 PROTEIN A-1 - HOMO SAPIENS (HUMAN), 304 aa.	5.90E-167	12
771	cg43329903	917	AGAATACCTGGG ACAAAGACACAG G[C/T]TGGAGGA CGAGGAGGACG AGGAAGA	C	T	Leu	Leu	SILENT-CODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q16664 PROTEIN A-1 - HOMO SAPIENS (HUMAN), 304 aa.	5.90E-167	12
772	cg43329903	952	AGGAGGACGAG GAAGAGGCTGAA GG[C/T]GGGGGG CTGGCCAGCCTT CGCCAAT	C	T	Gly	Gly	SILENT-CODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q16664 PROTEIN A-1 - HOMO SAPIENS (HUMAN), 304 aa.	5.90E-167	12
773	cg43949591	1809	TAAGAACACCTA TCCTGACTTCAT C[A/G]AGATCTTT TAAAAACCCATT AAAAA	A	G	Leu	Leu	SILENT-CODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAD43008 HYPOTHETICAL 19.5 KDA PROTEIN - HOMO SAPIENS (HUMAN), 367 aa.	2.60E-166	18
774	cg43949591	1812	GAACACCTATCC TGACTTCATCAA G[A/G]TCTTTTAA AAACCCATTAAA AATCG	A	G	Asp	Asp	SILENT-CODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAD43008 HYPOTHETICAL 19.5 KDA PROTEIN - HOMO SAPIENS (HUMAN), 367 aa.	2.60E-166	18
775	cg43949591	1824	TGACTTCATCAA GATCTTTTAAAAA [C/T]CCATTAAAA ATCGGAACCAGG TCTG	C	T	Gly	Gly	SILENT-CODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:AAD43008 HYPOTHETICAL 19.5 KDA PROTEIN - HOMO SAPIENS (HUMAN), 367 aa.	2.60E-166	18
776	cg43924431	1015	TTTCATTTTCATT CTCTTGAGCATT[C/T]TGTTCTATAT TATTAGCTACTT CAC	C	T	Gln	Gln	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:Q16637 SURVIVAL MOTOR NEURON PROTEIN 1 - Homo sapiens (Human), 294 aa.	4.20E-166	5

777	cg43951985	856	TGATTCCAGCATCATGGCAGGTATT[T/C]ACCACATCTGTCACATTCTTATAGG	T	C	Val	Val	SILENT-CODING	UNCLASSIFIED	Human Gene TREMBLNEW-ACC:CAB43357 HYPOTHETICAL 55.2 KD PROTEIN - HOMO SAPIENS (HUMAN), 505 aa.	2.50E-164	22
778	cg43949202	1179	TTGACTTCTCTTTTTCCAGTTCTTC[G/A]GCAAGGCCACAGGTGCAGTTCTTAC	G	A	Ala	Ala	SILENT-CODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75207 HYPOTHETICAL 33.6 KD PROTEIN - HOMO SAPIENS (HUMAN), 312 aa.	6.30E-163	16
779	cg43986422	891	CCTTTGTGTCCTTTCTTTTATTGAG[A/G]TCTTCAAACTGGCATTGAATATAGG	A	G	Asp	Asp	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:P04898 GUANINE NUCLEOTIDE-BINDING PROTEIN G(I), ALPHA-1 SUBUNIT (ADENYLATE CYCLASE-INHIBITING G ALPHA PROTEIN) - Homo sapiens (Human), and Bos taurus (Bovine), 353 aa.	6.30E-163	7 (7q21)
780	cg44015739	526	CATCACTGTCCGTGAGACCTATCCA[A/G]CGCGTGAAGGGGTTCGTGTGTTGTA	A	G	Arg	Arg	SILENT-CODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q03969 HEPATIC LECTIN H2, VARIANT (ASIALOGLYCOPROTEIN RECEPTOR H2) - HOMO SAPIENS (HUMAN), 287 aa.	2.80E-160	17 (17p)
781	cg43986534	766	ACTTCTGCTACGAATTCCCCTTCCC[G/C]CGGGTGGCCACCACCCCACCGCCCC	G	C	Pro	Pro	SILENT-CODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O75900 METALLOPROTEASE MMP21/22A - HOMO SAPIENS (HUMAN), 390 aa.	4.70E-160	
782	cg42720055	609	GAGGAGTGGCAGTATTCATTGGGCA[A/G]CCCACAGAGGTCGTGAAAGTCAGAC	A	G	Gln	Gln	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P25874 MITOCHONDRIAL BROWN FAT UNCOUPLING PROTEIN 1 (UCP 1) - *Homo sapiens (Human)*, 307 aa.	1.60E-157	
783	cg43287561	637	CAATCTGGCCTTTCTGCCGGGTTTC[C/A]GGATTCACTTTCTTCCTGGGAACAA	C	A	Pro	Pro	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:Q15526 SURFEIT LOCUS PROTEIN 1 - Homo sapiens (Human), 300 aa.	1.40E-156	9 (9q34)

784	cg43287561	661	CCGGATTCACTT TCTTCCTGGGAA C[A/G]AACCCTCT ATTGACCAGGAT GGTGA	A	G	Phe	Phe	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:Q15526 SURFEIT LOCUS PROTEIN 1 - Homo sapiens (Human), 300 aa.	1.40E-156	9 (9q34)
785	cg43287561	673	TCTTCCTGGGAA CAAACCCTCTAT T[G/T]ACCAGGAT GGTGACTCCCAA GTCAG	G	T	Val	Val	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:Q15526 SURFEIT LOCUS PROTEIN 1 - Homo sapiens (Human), 300 aa.	1.40E-156	9 (9q34)
786	cg43287561	693	CTATTGACCAGG ATGGTGACTCCC A[A/G]GTCAGAG CAATGGAAAGGA GTAACA	A	G	Leu	Leu	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:Q15526 SURFEIT LOCUS PROTEIN 1 - Homo sapiens (Human), 300 aa.	1.40E-156	9 (9q34)
787	cg43287561	697	TGACCAGGATGG TGACTCCCAAGT C[A/G]GAGCAAT GGAAAGGAGTAA CAACAT	A	G	Ser	Ser	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:Q15526 SURFEIT LOCUS PROTEIN 1 - Homo sapiens (Human), 300 aa.	1.40E-156	9 (9q34)
788	cg43287561	703	GGATGGTGACTC CCAAGTCAGAGC A[A/G]TGGAAAG GAGTAACAACAT AGGCCC	A	G	His	His	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:Q15526 SURFEIT LOCUS PROTEIN 1 - Homo sapiens (Human), 300 aa.	1.40E-156	9 (9q34)
789	cg43287561	709	TGACTCCCAAGT CAGAGCAATGGA A[A/G]GGAGTAA CAACATAGGCCC CACTTT	A	G	Pro	Pro	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:Q15526 SURFEIT LOCUS PROTEIN 1 - Homo sapiens (Human), 300 aa.	1.40E-156	9 (9q34)
790	cg43287561	715	CCAAGTCAGAGC AATGGAAAGGAG T[A/G]ACAACATA GGCCCCACTTTC AGTTG	A	G	Val	Val	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:Q15526 SURFEIT LOCUS PROTEIN 1 - Homo sapiens (Human), 300 aa.	1.40E-156	9 (9q34)

791	cg43287561	733	AAGGAGTAACAA CATAGGCCCCAC T[T/C]TCAGTTGA GGATAATCTGCC AGCAT	T	C	Glu	Glu	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:Q15526 SURFEIT LOCUS PROTEIN 1 - Homo sapiens (Human), 300 aa.	1.40E-156	9 (9q34)
792	cg43287561	769	ATAATCTGCCAG CATCACGTGCCT C[T/C]CGGACAG GGTCCACCATGG TCCGAG	T	C	Arg	Arg	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:Q15526 SURFEIT LOCUS PROTEIN 1 - Homo sapiens (Human), 300 aa.	1.40E-156	9 (9q34)
793	cg43287561	793	CTCGGACAGGG TCCACCATGGTC CG[A/G]GGCATT ATGTACAGCTCC TTGGAAT	A	G	Pro	Pro	SILENT-CODING	UNCLASSIFIED	Human Gene SWISSNEW-ACC:Q15526 SURFEIT LOCUS PROTEIN 1 - Homo sapiens (Human), 300 aa.	1.4E-156	9 (9q34)
794	cg43254730	1641	GTGGCTCATTCC AGAAGCTGAACT C[A/G]AGGAGCA GCTGGTTTCTCC TGGACA	A	G	Leu	Leu	SILENT-CODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:O43800 NIPSNAP1 PROTEIN - HOMO SAPIENS (HUMAN), 284 aa.	1.80E-156	22
795	cg43298828	424	TGATCTCAGCCT TCTGGATCTCCC C[A/G]TTCACATA CGGAGAGACTCT CAGAG	A	G	Asn	Asn	SILENT-CODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q92984 INTERFERON-INDUCED LEUCINE ZIPPER PROTEIN - HOMO SAPIENS (HUMAN), 299 aa (fragment).	1.10E-155	17
796	cg43060941	358	CTGCTGCTGTGT CCAGGCTCTCTT T[T/C]GCTTTCTC CACTATTTTATCT TTCA	T	C	Ala	Ala	SILENT-CODING	UNCLASSIFIED	Human Gene SPTREMBL-ACC:P70287 RETINOBLASTOMA BINDING PROTEIN 6 (PACT) - MUS MUSCULUS (MOUSE), 1587 aa (fragment).	4.90E-153	
797	cg43919239	407	CATGCATGGCTG CAGCATAGAACC T[C/A]GCCACTTC CTCGTTGGGGTT GCCCT	C	A	Ala	Ala	SILENT-CODING	UNCLASSIFIED	Human Gene Homologous to SWISSPROT-ACC:P14207 FOLATE RECEPTOR BETA PRECURSOR (FR-BETA) (FOLATE RÉCEPTOR 2) (FOLATE RECEPTOR, FETAL/PLACENTAL) (PLACENTAL FOLATE-BINDING PROTEIN) (FBP) - Homo sapiens (Human), 255 aa.	4.2E-150	

798	cg43917036	2502	TCGGGGAAATGTAGTACCAGTTGTT[G/C]GGCAGACGGAAAATGCGGTAATGCT	G	C	Pro	Pro	SILENT-CODING	UNCLASSIFIED	Human Gene Homologous to SPTREMBL-ACC:Q13239 PUTATIVE SRC-LIKE ADAPTER PROTEIN (SLAP) - HOMO SAPIENS (HUMAN), 276 aa.	1.30E-148	8
799	cg43927534	538	CCCGCTCCTGGGGGAGGTAGTCATG[G/A]CTGTGGGGCCCTGAGGTAGAGGGGC	G	A	Ser	Ser	SILENT-CODING	UNCLASSIFIED	Human Gene Homologous to SWISSPROT-ACC:P23249 PROTEIN MOV-10 - Mus musculus (Mouse), 1004 aa.	9.00E-148	1
800	cg43965796	1352	GGTCTGTTTGCATGAAGTGGAACTC[A/G]AACAGCTCCCTCAGGCACAGAACCA	A	G	Phe	Phe	SILENT-CODING	UNCLASSIFIED	Human Gene Homologous to SWISSPROT-ACC:Q60936 HYPOTHETICAL HEART PROTEIN - Mus musculus (Mouse), 298 aa (fragment).	9E-148	1
801	cg43950686	894	TGTCCCTTCAGTATTTCATCCCTGC[A/G]CTGTCCTAGCACCCTGTCGCTGGAG	A	G	Ala	Ala	SILENT-CODING	UNCLASSIFIED	Human Gene Homologous to SPTREMBL-ACC:O60921 HUS1+-LIKE PROTEIN - HOMO SAPIENS (HUMAN), 280 aa.	8.1E-147	
802	cg43971525	829	CTGGTGAGGCCATTTTCTCTCGCTT[T/C]TCCTGTTCAGCCTCCGGACCAATCA	T	C	Glu	Glu	SILENT-CODING	UNCLASSIFIED	Human Gene Homologous to SPTREMBL-ACC:O75337 LIPRIN-BETA2 - HOMO SAPIENS (HUMAN), 783 aa (fragment).	1.2E-143	11
803	cg43999829	665	GCCTGCTGTCACCAGGGGCGAGGCT[G/C]ATCACCATCGAGATCAACCCCGACT	G	C	Leu	Leu	SILENT-CODING	UNCLASSIFIED	Human Gene Homologous to SWISSPROT-ACC:P21964 CATECHOL O-METHYLTRANSFERASE, MEMBRANE-BOUND FORM (EC 2.1.1.6) (MB-COMT) [CONTAINS: CATECHOL O-METHYLTRANSFERASE, SOLUBLE FORM (S-COMT)] - Homo sapiens (Human), 271 aa.	2.1E-143	22 (22q11.2)

804	cg43308029	1020	ACAGTTACCGCG TGTACTACAATG C[C/A]GGCCCCA AGGATGAGGAC CAGGACT	C	A	Ala	Ala	SILENT-CODING	UNCLASSIFIED	Human Gene Homologous to SPTREMBL-ACC:O43819 CDNA HOMOLOGOUS TO YEAST SCO1 & SCO2 GENES AND C.ELEGANS C01F1.2 GENE - HOMO SAPIENS (HUMAN), 266 aa.	6.7E-143	22
805	cg43024858	413	GCGAGAGCAGC GACTTCGAATGC AA[T/C]CAGATGC TAGAGGCGCAG GAGGAGC	T	C	Asn	Asn	SILENT-CODING	UNCLASSIFIED	Human Gene Homologous to SPTREMBL-ACC:Q60438 HT PROTEIN - CRICETULUS GRISEUS (CHINESE HAMSTER), 348 aa.	2.3E-142	22
806	cg43309726	616	ACTGTAAGAAGG ACCTGCTCCGCC G[G/C]GACGTGC TGTACTACAAGG GCCGGC	G	C	Arg	Arg	SILENT-CODING	UNCLASSIFIED	Human Gene Homologous to TREMBLNEW-ACC:BAA83064 KIAA1112 PROTEIN - HOMO SAPIENS (HUMAN), 694 aa (fragment).	5E-136	
807	cg43309726	623	GAAGGACCTGCT CCGCCGGGACG TG[C/T]TGTACTA CAAGGGCCGGC TGGACAT	C	T	Leu	Leu	SILENT-CODING	UNCLASSIFIED	Human Gene Homologous to TREMBLNEW-ACC:BAA83064 KIAA1112 PROTEIN - HOMO SAPIENS (HUMAN), 694 aa (fragment).	5E-136	
808	cg43994220	323	TCGGGGTGTAG CCAGAGTCGGCT TC[G/A]GTGGTG AGGTCAGCGCCT CGGGCCA	G	A	Thr	Thr	SILENT-CODING	UNCLASSIFIED	Human Gene Homologous to SWISSNEW-ACC:O14593 DNA-BINDING PROTEIN RFXANK - Homo sapiens (Human), 260 aa.	5.8E-135	19
809	cg43948495	1189	TCCTACTCCTCC GTTCCTCATATG G[G/T]GAATGGG TTGTCCTCCCAC GGTCAC	G	T	Ser	Ser	SILENT-CODING	UNCLASSIFIED	Human Gene Homologous to SPTREMBL-ACC:Q13722 UNKNOWN PROTEIN - HOMO SAPIENS (HUMAN), 256 aa.	9.7E-135	3
810	cg43942432	811	TGTACTGCAGGG GATGCTCTGCCG G[C/T]CCAGGGA CAACAGCCTTTC TCTTGC	C	T	Gly	Gly	SILENT-CODING	UNCLASSIFIED	Human Gene Homologous to SPTREMBL-ACC:O60573 CAP-BINDING PROTEIN 4EHP - HOMO SAPIENS (HUMAN), 245 aa.	5.30E-134	2

811	cg42910848	319	CGCAACACTAGAGACGTCTTCTGGC[T/C]GCCATCAGGGGACTCGGAGGTAGGG	T	C	Ala	Ala	SILENT-CODING	UNCLASSIFIED	Human Gene Homologous to SPTREMBL-ACC:O14988 GTPASE-ACTIVATING PROTEIN - HOMO SAPIENS (HUMAN), 308 aa (fragment).	3.10E-132	
812	cg42910848	484	TGAAGATCTTTTCATAGTACTCGAT[C/T]AGCAGTTCAGTGAACATGTTCAGGG	C	T	Leu	Leu	SILENT-CODING	UNCLASSIFIED	Human Gene Homologous to SPTREMBL-ACC:O14988 GTPASE-ACTIVATING PROTEIN - HOMO SAPIENS (HUMAN), 308 aa (fragment).	3.10E-132	
813	cg43918679	330	TGACGCGGAAGATGGTTCTGACCCG[G/A]GCCAAGGCCTCGGAGCTGCACAGCG	G	A	Arg	Arg	SILENT-CODING	UNCLASSIFIED	Human Gene Homologous to SWISSPROT-ACC:O43822 28.3 KD PROTEIN C21ORF2 (C21ORF-HUMF09G8.5) (YF5/A2) - Homo sapiens (Human), 256 aa.	3.00E-131	21
814	cg43918152	356	AAAGTAATGGTCCAACAGACAGTTA[C/T]GCAGCCATTTCAGAAGTGGATCGAT	C	T	Tyr	Tyr	SILENT-CODING	UNCLASSIFIED	Human Gene Homologous to SWISSPROT-ACC:P09496 CLATHRIN LIGHT CHAIN A (BRAIN AND LYMPHOCYTE LCA) - Homo sapiens (Human), 248 aa.	5.00E-131	9 (12q23)
815	cg43918152	362	ATGGTCCAACAGACAGTTACGCAGC[C/T]ATTTCAGAAGTGGATCGATTGCAGT	C	T	Ala	Ala	SILENT-CODING	UNCLASSIFIED	Human Gene Homologous to SWISSPROT-ACC:P09496 CLATHRIN LIGHT CHAIN A (BRAIN AND LYMPHOCYTE LCA) - Homo sapiens (Human), 248 aa.	5.00E-131	9 (12q23)
816	cg43918152	431	GTAAATGGAGAGAAGAACAAACGGA[G/A]CGCTTGGAAGCCCTCGATGCCAATT	G	A	Glu	Glu	SILENT-CODING	UNCLASSIFIED	Human Gene Homologous to SWISSPROT-ACC:P09496 CLATHRIN LIGHT CHAIN A (BRAIN AND LYMPHOCYTE LCA) - Homo sapiens (Human), 248 aa.	5.00E-131	9 (12q23)
817	cg43918152	446	AACAAACGGAGCGCTTGGAAGCCCT[C/T]GATGCCAATTCTCGGAAGCAAGAAG	C	T	Leu	Leu	SILENT-CODING	UNCLASSIFIED	Human Gene Homologous to SWISSPROT-ACC:P09496 CLATHRIN LIGHT CHAIN A (BRAIN AND LYMPHOCYTE LCA) - Homo sapiens (Human), 248 aa.	5.00E-131	9 (12q23)

818	cg43918152	503	GGAAAGAAAAGG CAATAAAGGAGC T[G/A]GAAGAGT GGTATGCGAGG CAGGACG	G	A	Leu	Leu	SILENT-CODING	UNCLASSIFIED	Human Gene Homologous to SWISSPROT-ACC:P09496 CLATHRIN LIGHT CHAIN A (BRAIN AND LYMPHOCYTE LCA) - Homo sapiens (Human), 248 aa.	5.00E-131	9 (12q23)
819	cg43918152	509	AAAAGGCAATAA AGGAGCTGGAA GA[G/A]TGGTATG CGAGGCAGGAC GAGCAGC	G	A	Glu	Glu	SILENT-CODING	UNCLASSIFIED	Human Gene Homologous to SWISSPROT-ACC:P09496 CLATHRIN LIGHT CHAIN A (BRAIN AND LYMPHOCYTE LCA) - Homo sapiens (Human), 248 aa.	5.00E-131	9 (12q23)
820	cg43918152	518	TAAAGGAGCTGG AAGAGTGGTATG C[G/A]AGGCAGG ACGAGCAGCTAC AGAAGA	G	A	Ala	Ala	SILENT-CODING	UNCLASSIFIED	Human Gene Homologous to SWISSPROT-ACC:P09496 CLATHRIN LIGHT CHAIN A (BRAIN AND LYMPHOCYTE LCA) - Homo sapiens (Human), 248 aa.	5.00E-131	9 (12q23)
821	cg43918152	521	AGGAGCTGGAA GAGTGGTATGCG AG[G/A]CAGGAC GAGCAGCTACAG AAGACAA	G	A	Arg	Arg	SILENT-CODING	UNCLASSIFIED	Human Gene Homologous to SWISSPROT-ACC:P09496 CLATHRIN LIGHT CHAIN A (BRAIN AND LYMPHOCYTE LCA) - Homo sapiens (Human), 248 aa.	5.00E-131	9 (12q23)
822	cg43918152	542	CGAGGCAGGAC GAGCAGCTACAG AA[G/A]ACAAAGG CAAACAACAGGG TGGCAG	G	A	Lys	Lys	SILENT-CODING	UNCLASSIFIED	Human Gene Homologous to SWISSPROT-ACC:P09496 CLATHRIN LIGHT CHAIN A (BRAIN AND LYMPHOCYTE LCA) - Homo sapiens (Human), 248 aa.	5.00E-131	9 (12q23)
823	cg43918152	548	AGGACGAGCAG CTACAGAAGACA AA[G/A]GCAAACA ACAGGGTGGCA GATGAAG	G	A	Lys	Lys	SILENT-CODING	UNCLASSIFIED	Human Gene Homologous to SWISSPROT-ACC:P09496 CLATHRIN LIGHT CHAIN A (BRAIN AND LYMPHOCYTE LCA) - Homo sapiens (Human), 248 aa.	5.00E-131	9 (12q23)
824	cg43928955	182	ACTCTTATGTGA AGTCTACCAAGC T[T/C]GTGCTCAA GGGAACCAAGG CGAAGA	T	C	Leu	Leu	SILENT-CODING	UNCLASSIFIED	Human Gene Homologous to SPTREMBL-ACC:Q14331 FRG1 - HOMO SAPIENS (HUMAN), 258 aa.	1.30E-129	

825	cg43917824	584	CAGTGGTGGTGTTCAGATTTTTCCA[A/G]GAATTACCAGGCTCAGATCCGGTGT	A	G	Gln	Gln	SILENT-CODING	UNCLASSIFIED	Human Gene Homologous to SPTREMBL-ACC:O00236 KIAA0251 - HOMO SAPIENS (HUMAN), 820 aa (fragment).	1.30E-128	16
826	cg43917824	674	TCGGCCGGGAGAGGCACTCGTGTGA[T/C]GCGCTGAATCGCTGGCTGGGAGAAC	T	C	Asp	Asp	SILENT-CODING	UNCLASSIFIED	Human Gene Homologous to SPTREMBL-ACC:O00236 KIAA0251 - HOMO SAPIENS (HUMAN), 820 aa (fragment).	1.30E-128	16
827	cg44128041	132	GGCAGTATGAGAACAGCGAAGGGGG[T/C]TGGATGGAGGACTATGACTACGTTC	T	C	Gly	Gly	SILENT-CODING	UNCLASSIFIED	Human Gene Homologous to SPTREMBL-ACC:Q61140 V-CRK-ASSOCIATED TYROSINE KINASE SUBSTRATE P130CAS - MUS MUSCULUS (MOUSE), 874 aa.	2.80E-128	
828	cg43926784	1062	ATACAAGCCATTCATAAACCTCATC[G/A]CTGATGCAGAGTGTGTCATATTTGA	G	A	Ser	Ser	SILENT-CODING	UNCLASSIFIED	Human Gene Homologous to TREMBLNEW-ACC:CAB44334 CYSTEINE CONJUGATE BETA-LYASE - FUGU RUBRIPES (JAPANESE PUFFERFISH) (TAKIFUGU RUBRIPES), 419 aa.	6.70E-127	
829	cg43995142	894	ACAGTGAGATGGCTGGGAAGTAAAC[C/A]CCCTCAAAAATATCTTTGTAAGCCA	C	A	Gly	Gly	SILENT-CODING	UNCLASSIFIED	Human Gene Homologous to SPTREMBL-ACC:O60660 ASH2L1 - HOMO SAPIENS (HUMAN), 628 aa.	8.00E-127	
830	cg43975901	682	CAGTTAAAGGCGTCACAGGACATGA[A/G]GTCTGCAATTATTTCTGGAATGTTG	A	G	Glu	Glu	SILENT-CODING	UNCLASSIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD30288 GOODPASTURE ANTIGEN-BINDING PROTEIN (EC 2.7.1.37) - HOMO SAPIENS (HUMAN), 624 aa.	2.60E-125	
831	cg43307940	788	GATCAAGTCCCTCACCTATACGGCA[A/T]ATTCTGTTGTTGTTCACTAACAATG	A	T	Ile	Ile	SILENT-CODING	UNCLASSIFIED	Human Gene Homologous to SWISSNEW-ACC:P09661 U2 SMALL NUCLEAR RIBONUCLEOPROTEIN A' (U2 SNRNP-A') - Homo sapiens (Human), 255 aa.	8.10E-125	15

832	cg44028574	1607	AGGCCGAGTTCA GCCTTCTGCAGG A[A/G]CATCTGG GTGAGGGTCCA GCGAATG	A	G	Cys	Cys	SILENT-CODING	UNCLASSIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD27724 CGI-15 PROTEIN - HOMO SAPIENS (HUMAN), 329 aa.	4.00E-122	20
833	cg43958446	421	CGGGGCCATCT CAGATGGTCTCA TC[A/G]TCGCTCA TGTCCCAGATCT CAGCAG	A	G	Asp	Asp	SILENT-CODING	UNCLASSIFIED	Human Gene Homologous to SPTREMBL-ACC:O43069 HYPOTHETICAL 73.5 KD PROTEIN - SCHIZOSACCHAROMYCES POMBE (FISSION YEAST), 650 aa.	3.10E-120	
834	cg44002087	380	AATTCAACAACG AAATCAATATGA A[C/A]GAAAAGGT GAAAAGGCACCA AAGCT	C	A	Arg	Arg	SILENT-CODING	UNCLASSIFIED	Human Gene Homologous to SPTREMBL-ACC:O60712 HYPOTHETICAL 26.9 KD PROTEIN - HOMO SAPIENS (HUMAN), 236 aa.	2.90E-119	
835	cg29350504	989	CTGTAATAGATT CCTCACTGCTTG A[A/C]AGGCTTTC TATGGTCTCCCT TGCAA	A	C	Leu	Leu	SILENT-CODING	UNCLASSIFIED	Human Gene Homologous to SWISSPROT-ACC:P05814 BETA CASEIN PRECURSOR - Homo sapiens (Human), 226 aa.	4.70E-119	4 (4q21.1)
836	cg43067745	180	TCCCTACCTTAG AAGAAGGGAGG TG[G/A]TAGATGA AATGAACTGTAT GAAGAG	G	A	Tyr	Tyr	SILENT-CODING	UNCLASSIFIED	Human Gene Homologous to SPTREMBL-ACC:O75839 TSC501 PROTEIN - HOMO SAPIENS (HUMAN), 227 aa.	6.90E-118	
837	cg43067745	210	TGAAATGAACTG TATGAAGAGCCA C[T/C]AGCCTGG CCCACACACAGA AGAAGG	T	C	Leu	Leu	SILENT-CODING	UNCLASSIFIED	Human Gene Homologous to SPTREMBL-ACC:O75839 TSC501 PROTEIN - HOMO SAPIENS (HUMAN), 227 aa.	6.90E-118	
838	cg43067745	225	GAAGAGCCACTA GCCTGGCCCAC AC[A/G]CAGAAG AAGGACTGGCC CGTCTTCT	A	G	Cys	Cys	SILENT-CODING	UNCLASSIFIED	Human Gene Homologous to SPTREMBL-ACC:O75839 TSC501 PROTEIN - HOMO SAPIENS (HUMAN), 227 aa.	6.90E-118	

839	cg43919033	1463	CCGTGGGTTCCC CGAGGCTCTGTG G[C/T]GTGGGCA TGCAGGCGTAGT TCCATT	C	T	Thr	Thr	SILENT-CODING	UNCLASSIFIED	Human Gene Homologous to TREMBLNEW-ACC:CAB46693 DJ797M17.1 (DERMATOPONTIN) - HOMO SAPIENS (HUMAN), 201 aa.	6.20E-117	1 (1q12)
840	cg43919033	1511	ATTGTCTGTCAG AACCTTCCTTCT T[G/A]CTGAAGAT GCTCCTCACGGC CACTA	G	A	Ser	Ser	SILENT-CODING	UNCLASSIFIED	Human Gene Homologous to TREMBLNEW-ACC:CAB46693 DJ797M17.1 (DERMATOPONTIN) - HOMO SAPIENS (HUMAN), 201 aa.	6.20E-117	1 (1q12)
841	cg43919033	1577	GACACTGGTAGC TGAAGCCTTGCC G[G/A]TTCAAATT CACCCACCCATC ATCGC	G	A	Asn	Asn	SILENT-CODING	UNCLASSIFIED	Human Gene Homologous to TREMBLNEW-ACC:CAB46693 DJ797M17.1 (DERMATOPONTIN) - HOMO SAPIENS (HUMAN), 201 aa.	6.20E-117	1 (1q12)
842	cg43948724	1702	CATCTCATGAGT GTGCCCCATGG GT[C/T]CCCTCCC CTCTCAGCATTT CCTTGT	C	T	Val	Val	SILENT-CODING	UNCLASSIFIED	Human Gene Homologous to SWISSPROT-ACC:P26442 AUTOCRINE MOTILITY FACTOR RECEPTOR PRECURSOR (AMF RECEPTOR) (GP78) - *Homo sapiens* (Human), 323 aa.	9.90E-114	16 (16q21)
843	cg43036790	144	CTGTAACATCTT CCTCTTCCCCAT C[G/A]GGGTTGA ATCTATTGAAAT GTATAC	G	A	Pro	Pro	SILENT-CODING	UNCLASSIFIED	Human Gene Homologous to SPTREMBL-ACC:O75058 KIAA0470 PROTEIN - HOMO SAPIENS (HUMAN), 1460 aa.	1.50E-110	
844	cg43325007	854	ACGGGTCCCAC CTGGGTTCAGG GAT[G/A]TAGCCC TTCTCTACAGCC AGGCGGC	G	A	Tyr	Tyr	SILENT-CODING	UNCLASSIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD43195 PEROXISOMAL MEMBRANE PROTEIN PMP 24 - HOMO SAPIENS (HUMAN), 212 aa.	4.80E-110	20
845	cg42907145	903	GGCACTTCTCGG ACTCTCCAAACT T[C/T]GCAGTGAA TTTGGAAGGGTT GCTGG	C	T	Ala	Ala	SILENT-CODING	UNCLASSIFIED	Human Gene Homologous to SWISSPROT-ACC:P50461 LIM DOMAIN PROTEIN, CARDIAC (MUSCLE LIM PROTEIN) (CYSTEINE-RICH PROTEIN 3) (CRP3) (LIM-ONLY PROTEIN 4) - Homo sapiens (Human), 194 aa.	1.10E-108	11

846	cg43296554	173	CGGTACACGGTC GTCTCTCTCCTG C[C/T]CTCATCAG TGGCCTTCTCTC TTGGG	C	T	Arg	Arg	SILENT-CODING	UNCLASSIFIED	Human Gene Homologous to SWISSNEW-ACC:Q15527 SURFEIT LOCUS PROTEIN 2 - Homo sapiens (Human), 256 aa.	6.40E-108	9
847	cg43997383	293	TCGAGGACCTGT CTGAAGACTTGG A[A/G]TGGAAAAT TATCTATGTGGG CTCTG	A	G	Glu	Glu	SILENT-CODING	UNCLASSIFIED	Human Gene Homologous to TREMBLNEW-ACC:CAB43363 HYPOTHETICAL 23.0 KD PROTEIN - HOMO SAPIENS (HUMAN), 204 aa.	8.00E-108	
848	cg43941085	500	GGGCCTGGGTTT GCTCCCAGTTTC C[G/T]GGCTACC GAGGATTTCAGT ATGTGC	G	T	Pro	Pro	SILENT-CODING	UNCLASSIFIED	Human Gene Homologous to SWISSPROT-ACC:P53673 BETA CRYSTALLIN A4 - Homo sapiens (Human), 195 aa.	8.10E-108	22 (22q11.2)
849	cg43947512	425	TCAACAGGTTAG GAGAGTTGATCC T[C/T]ACCTCTGA GAGCAGCCGCT ATCAGT	C	T	Leu	Leu	SILENT-CODING	UNCLASSIFIED	Human Gene Homologous to SWISSNEW-ACC:Q14197 DS-1 PROTEIN - Homo sapiens (Human), 206 aa.	2.10E-107	17
850	cg43947512	570	TCATAGAATCAG GATAGAAAACAT G[C/A]NTCGGGA AAGGCTGAGACA AAAGAG	C	A	???	???	SILENT-CODING	UNCLASSIFIED	Human Gene Homologous to SWISSNEW-ACC:Q14197 DS-1 PROTEIN - Homo sapiens (Human), 206 aa.	2.10E-107	17
851	cg43979124	1071	CTCATCAAAGGA ATGCACTAGGAT T[C/T]GCGCGGG GGTCTTTCTGGT TCCTGT	C	T	Ala	Ala	SILENT-CODING	UNCLASSIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD43023 TRANSMEMBRANE 4 SUPERFAMILY PROTEIN - HOMO SAPIENS (HUMAN), 204 aa.	2.10E-107	
852	cg43945125	680	AGGACTTGTTGT GGTACGTGCCTC G[C/G]GCCAGCA TGCCCTTGGGAG CCTCCT	C	G	Ala	Ala	SILENT-CODING	UNCLASSIFIED	Human Gene Homologous to SWISSPROT-ACC:P52566 RHO GDP-DISSOCIATION INHIBITOR 2 (RHO GDI 2) (RHO-GDI BETA) (LY-GDI) - Homo sapiens (Human), 201 aa.	2.70E-107	12

853	cg42854459	287	AGGGTAACCGCA AGTACTTGGTGA C[A/G]TTATGGAG GTTTATGGCATA CAGAG	A	G	Asn	Asn	SILENT-CODING	UNCLASSIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD41342 HEPARANASE - HOMO SAPIENS (HUMAN), 543 aa.	3.50E-107	
854	cg42923937	543	CCAGGTCCAGG GGGTAGGTCAGT GA[A/T]GCGGCT GTCGTTCCAGCC AGTGCGC	A	T	Ala	Ala	SILENT-CODING	UNCLASSIFIED	Human Gene Homologous to SPTREMBL-ACC:O43378 R29893_1 - HOMO SAPIENS (HUMAN), 216 aa (fragment).	4.40E-107	
855	cg42365149	259	TGGCGAACCACA GCCAGGACTGC GC[G/A]CCGCCG GCCCGGCGCCG GCTCACCT	G	A	Gly	Gly	SILENT-CODING	UNCLASSIFIED	Human Gene Homologous to TREMBLNEW-ACC:BAA77398 TEN-M3 - MUS MUSCULUS (MOUSE), 2715 aa.	1.70E-105	
856	cg43991689	686	GGGCTTCGGTGT TGAACACGTAGG C[A/G]TCCAGGC TGAGCAGGTTTG GGTCAT	A	G	Asp	Asp	SILENT-CODING	UNCLASSIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD45504 ENDOPLASMIC RETICULUM ALPHA-MANNOSIDASE I (EC 3.2.1.113) - HOMO SAPIENS (HUMAN), 663 aa.	2.50E-104	
857	cg43963123	1595	AGAACTTGACCG TGGTCACAGTTC T[A/G]CCACCCTG GACCCTCTCGGT GGCCT	A	G	Gly	Gly	SILENT-CODING	UNCLASSIFIED	Human Gene Homologous to SPTREMBL-ACC:O00588 RADICAL FRINGE - HOMO SAPIENS (HUMAN), 191 aa (fragment).	6.70E-104	17
858	cg43972159	1519	TGGCCGCCATCA CCTTCTTGATGT C[A/G]TCCTTGGC CCGGCTACGGG TCTCGG	A	G	Asp	Asp	SILENT-CODING	UNCLASSIFIED	Human Gene Homologous to SPTREMBL-ACC:Q13845 BCL7B PROTEIN - HOMO SAPIENS (HUMAN), 202 aa.	2.60E-102	7 (12q24.1).
859	cg43943283	1114	ATGTGAGCGAAT TGGGCCTTGTGA C[A/G]CAAGGAG GCAAAGTTATTT GGGGAA	A	G	Thr	Thr	SILENT-CODING	UNCLASSIFIED	Human Gene Homologous to SPTREMBL-ACC:O76994 INTRONIC PROTEIN 259 - DROSOPHILA MELANOGASTER (FRUIT FLY), 259 aa.	1.10E-101	5

860	cg43980312	2517	CTTCGGCTGGGTCCATTTTCCTTTC[T/A]GAGTCAGAGAGGTGAACTTTCTCTT	T	A	Ser	Ser	SILENT-CODING	UNCLASSIFIED	Human Gene Homologous to SWISSPROT-ACC:P34741 SYNDECAN-2 PRECURSOR (FIBROGLYCAN) (HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN) (HSPG) (SYND2) - Homo sapiens (Human), 201 aa.	7.90E-101	8 (8q22)
861	cg42028329	109	CGGCGGCCAAGGAGAACCCGTGCAG[A/G]AAATTCCAGGCCAACATCTTCAACA	A	G	Arg	Arg	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to SPTREMBL-ACC:P97434 P116RIP - MUS MUSCULUS (MOUSE), 1024 aa.	2.40E-99	
862	cg42028329	220	TGACGCAGGCAAAACCCATTTATGG[T/C]GGCTGGCTGCTCCTGGCTCCAGATG	T	C	Gly	Gly	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to SPTREMBL-ACC:P97434 P116RIP - MUS MUSCULUS (MOUSE), 1024 aa.	2.40E-99	
863	cg42028329	223	CGCAGGCAAAACCCATTTATGGTGG[C/T]TGGCTGCTCCTGGCTCCAGATGGCA	C	T	Gly	Gly	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to SPTREMBL-ACC:P97434 P116RIP - MUS MUSCULUS (MOUSE), 1024 aa.	2.40E-99	
864	cg42028329	247	GCTGGCTGCTCCTGGCTCCAGATGG[C/G]ACCGACTTTGACAACCCAGTACACC	C	G	Gly	Gly	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to SPTREMBL-ACC:P97434 P116RIP - MUS MUSCULUS (MOUSE), 1024 aa.	2.40E-99	
865	cg42028329	268	ATGGCACCGACTTTGACAACCCAGT[A/G]CACCGGTCTCGGAAATGGCAGCGAC	A	G	Val	Val	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to SPTREMBL-ACC:P97434 P116RIP - MUS MUSCULUS (MOUSE), 1024 aa.	2.40E-99	
866	cg42646578	422	ACCGATCACGGTTTTCAAAGTCTCT[G/A]TGAGCATATCTTGCATAAGTCTTGT	G	A	His	His	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to TREMBLNEW-ACC:AAD31085 KU70-BINDING PROTEIN - HOMO SAPIENS (HUMAN), 288 aa (fragment).	2.40E-99	

867	cg43925352	207	AGGAGTTGCAGC GGCGGCTGAAG CG[C/T]CTCTACC CGGCCGTGGAC GAACAAG	C	T	Arg	Arg	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to SPTREMBL-ACC:O60738 KB07 PROTEIN - HOMO SAPIENS (HUMAN), 243 aa (fragment).	3.70E-97	6
868	cg43961552	454	TCATGTTGGCGA GCTATTTCCTTAT [C/A]TCCATGTTT GGAGGAGTCAT GGTCT	C	A	Ile	Ile	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to SPTREMBL-ACC:O75915 JWA PROTEIN - HOMO SAPIENS (HUMAN), 188 aa.	2.80E-96	3
869	cg43935925	597	GAGTACTCTCCA GAGGCTGGAGG TT[C/T]GTGCGGA GTTTGTACATGT GGTTGA	C	T	Thr	Thr	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to TREMBLNEW-ACC:AAD34117 CGI-122 PROTEIN - HOMO SAPIENS (HUMAN), 185 aa.	4.60E-96	16
870	cg43971745	1560	GAGGGTCCTCA GGCTCAGGGGT CTG[G/C]CCGCC AGGGTGGGGAT GGGAGTGAG	G	C	Gly	Gly	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to SWISSPROT-ACC:P41271 ZINC FINGER PROTEIN DAN (N03) - Homo sapiens (Human), 180 aa.	2.00E-95	1
871	cg43922566	874	CACCAGGTGCCT CTGCAACAATGA A[A/G]TACTCTGG CCAGTGGGCGA GGTATT	A	G	Tyr	Tyr	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to TREMBLNEW-ACC:AAD40190 N-TERMINAL ACETYLTRANSFERASE COMPLEX ARD1 SUBUNIT - HOMO SAPIENS (HUMAN), 178 aa.	3.40E-93	20
872	cg43968495	1510	CCAAGTCTACCT CTGGGGGGACG CC[T/C]GGCTCA GCCCCCGCAGA CCTGCCCA	T	C	Pro	Pro	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to TREMBLNEW-ACC:CAB50743 HNRNP-E2 PROTEIN - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 353 aa.	3.40E-92	3
873	cg43955549	1295	GACTATGAGCAA AGGAACAGTTTC C[A/C]ACATATTG ACATTTTTCCCA GAAG	A	C	Val	Val	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to TREMBLNEW-ACC:BAA82983 KIAA1031 PROTEIN - HOMO SAPIENS (HUMAN), 940 aa (fragment).	1.70E-91	16

874	cg43978148	805	TAAACAACCTCC TGCACAGTCTGC A[A/G]CTTCCTGA GGCCTGTTCTGA AATAA	A	G	Gln	Gln	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to SPTREMBL-ACC:O75201 HYPOTHETICAL 64.6 KD PROTEIN - HOMO SAPIENS (HUMAN), 580 aa (fragment).	4.00E-90	16
875	cg42341305	100	AACAGACTTTGC CAGATGAATATT C[G/C]AGTACAG ACACACCGTATC CCGGCA	G	C	Ser	Ser	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to SPTREMBL-ACC:O60309 KIAA0563 PROTEIN - HOMO SAPIENS (HUMAN), 870 aa.	8.10E-90	
876	cg42341305	124	CGAGTACAGACA CACCGTATCCCG G[C/T]AGCCTACC TCCAGAACTCCG GGTGA	C	T	Gly	Gly	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to SPTREMBL-ACC:O60309 KIAA0563 PROTEIN - HOMO SAPIENS (HUMAN), 870 aa.	8.10E-90	
877	cg42341305	130	CAGACACACCGT ATCCCGGCAGC CT[A/G]CCTCCAG AACTCCGGGTGA AGGCAG	A	G	Leu	Leu	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to SPTREMBL-ACC:O60309 KIAA0563 PROTEIN - HOMO SAPIENS (HUMAN), 870 aa.	8.10E-90	
878	cg42463588	275	TTATTAATTCAAA GGCATCTCTGAC [A/G]TATGCTGAA GCTCAGTTGAGA ATTG	A	G	Thr	Thr	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to TREMBLNEW-ACC:BAA76852 KIAA1008 PROTEIN - HOMO SAPIENS (HUMAN), 928 aa.	8.20E-90	
879	cg43924895	200	AGGTTGGAGATC TCATCTATGGCC A[G/A]TTTGTGGT TGCTAATAAAGA CATGG	G	A	Gln	Gln	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to TREMBLNEW-ACC:AAD34097 CGI-102 PROTEIN - HOMO SAPIENS (HUMAN), 220 aa.	1.30E-89	9
880	cg43969092	638	GGCCGGCCATC AGCACGCCCTTC AC[G/C]CGTTCCT CCTCCTCACTGC ACTCGT	G	C	Arg	Arg	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to TREMBLNEW-ACC:BAA74913 KIAA0890 PROTEIN - HOMO SAPIENS (HUMAN), 1194 aa.	6.30E-89	

881	*cg43955651*	*521*	CACACTCTCTGTGCATCGGCTTGCG[C/T]GTGTCCGGGTGGAAGGAGTTGAACG	C	T	Thr	Thr	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to TREMBLNEW-ACC:AAD27745 CGI-36 PROTEIN - HOMO SAPIENS (HUMAN), 165 aa.	1.10E-87	2
882	cg43970868	507	TCTGGCTCTGGGATATTCTGGCCTC[C/T]GACTTCACACCGGATGAGAGAGCTA	C	T	Ser	Ser	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to TREMBLNEW-ACC:CAA19508 Y39A1C.2 PROTEIN - CAENORHABDITIS ELEGANS, 1066 aa.	9.80E-87	12
883	cg43068353	456	AAAATCCTTCTTTGGTTGACTTAAA[T/C]TCTGTATTAGAAGAACCCTTTGTGG	T	C	Glu	Glu	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to SWISSPROT-ACC:P49792 NUCLEAR PORE COMPLEX PROTEIN NUP358 (NUCLEOPORIN NUP358) (358 KD NUCLEOPORIN) (P270) (RAN-BINDING PROTEIN 2) - Homo sapiens (Human), 3224 aa.	1.00E-86	2
884	cg43250258	123	AAATGATAGCATCCAATAATGTCCC[G/A]ATACTTTCTTCTTGTGAAGAGAGTT	G	A	Ile	Ile	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to TREMBLNEW-ACC:AAD34116 CGI-121 PROTEIN - HOMO SAPIENS (HUMAN), 175 aa.	2.60E-86	2
885	cg43934734	1040	GTATGGAAATCTCATCCGGCTCCCC[C/T]TGGTACTCCGGCAGGTCAATTTTCT	C	T	Gln	Gln	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to SPTREMBL-ACC:O14878 PUTATIVE ONCOGENE PROTEIN - HOMO SAPIENS (HUMAN), 157 aa (fragment).	7.10E-84	20
886	cg43934734	617	GTCAAGCTGCCAAACTGCCAAAGTA[C/T]TCCTGCAGCTCCAGCAGGGCCCGGA	C	T	Glu	Glu	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to SPTREMBL-ACC:O14878 PUTATIVE ONCOGENE PROTEIN - HOMO SAPIENS (HUMAN), 157 aa (fragment).	7.10E-84	20
887	cg43996941	396	TTGCACTAAAAGGATCTGTAGCTTT[T/C]CCAGCTGAGAATGGAGTTCAGAATA	T	C	Phe	Phe	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to SPTREMBL-ACC:Q16044 PREPRO-MELANIN-CONCENTRATING HORMONE - HOMO SAPIENS (HUMAN), 165 aa.	3.10E-83	12 (12q23)

888	cg43989507	273	GCAGGAGTGGA AACCAGTAGCTG TC[G/A]TCGGGC CACATGTCCTTG AAGGGGA	G	A	Asp	Asp	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to SWISSPROT-ACC:P36639 7,8-DIHYDRO-8-OXOGUANINE TRIPHOSPHATASE (EC 3.1.6.-) (8-OXO-DGTPASE) - Homo sapiens (Human), 156 aa.	3.90E-83	7 (7p22)
889	cg43970119	426	CCATTAGTAGGC AAATGTGCTCTG C[G/A]AATTCTCG GATGGCACCAC GGCCAC	G	A	Phe	Phe	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to SPTREMBL-ACC:O88719 CMP-N-ACETYLNEURAMINIC ACID SYNTHETASE (EC 2.7.7.43) (ACYLNEURAMINATE CYTIDYLYLTRANSFERASE) (CMP-SIALATE PYROPHOSPHORYLASE) (CMP-SIALATE SYNTHASE) - MUS MUSCULUS (MOUSE), 432 aa.	1.00E-82	12
890	cg43120215	1007	GGCAGCACTTG GACAGGATGCTG AA[G/C]CCGGCT GCAATGAAGATG AC	G	C	Gly	Gly	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to SPTREMBL-ACC:P78524 P126 (P70) - HOMO SAPIENS (HUMAN), 1137 aa.	1.30E-82	7
891	cg44007579	95	GCTACCGCAGC CGCTGGTTCGTG TT[C/T]GACGCGC GCCGCTGCTACC TTTTACT	C	T	Phe	Phe	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to TREMBLNEW-ACC:BAA83007 KIAA1055 PROTEIN - HOMO SAPIENS (HUMAN), 868 aa (fragment).	2.20E-82	
892	cg43322319	622	ATGCCTACAAGA CTATGAAAGAGG A[C/T]GAAAAAAG ATACAATGAAAG AATTT	C	T	Asp	Asp	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to TREMBLNEW-ACC:CAB41267 HYPOTHETICAL 66.3 KD PROTEIN - HOMO SAPIENS (HUMAN), 609 aa.	1.20E-81	
893	cg43917139	113	CTTGGCTGGTGG CCGGCTTGGGTT T[C/T]GCTTGTAC ATTCAGCACATA ATCAT	C	T	Ala	Ala	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to TREMBLNEW-ACC:BAA76671 CARBONIC ANHYDRASE VB - HOMO SAPIENS (HUMAN), 317 aa.	2.50E-81	X
894	cg43321624	660	AATAACGTGGAT TATGAGGGGCCT C[G/A]GTCACAG CCTGCAGTTCGT AGGGGA	G	A	Thr	Thr	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to SPTREMBL-ACC:O60377 P1.11659_5 - HOMO SAPIENS (HUMAN), 188 aa (fragment).	1.10E-80	9

895	cg42903644	671	TGGTGCCTGTCA GCAAGCCCGGT GC[A/C]CTTCGTC GCTCCCTGTCCC GCTCCA	A	C	Ala	Ala	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to SWISSPROT-ACC:O15273 TELETHONIN - Homo sapiens (Human), 167 aa.	1.40E-80	17
896	cg43969140	425	CAAAGATGGACA CCAGCGAATCAT C[T/C]AGTAATAA GTCTGTCTCCTT CCCAA	T	C	Leu	Leu	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to SWISSPROT-ACC:P30044 PUTATIVE PEROXISOMAL ANTIOXIDANT ENZYME (LIVER TISSUE 2D-PAGE SPOT 71B) - Homo sapiens (Human), 161 aa.	1.70E-80	
897	cg43969140	515	CCGCCTTGTGG GCTCGGCCCCA CTC[G/T]CCAGTC ACAAAGGCATCA TTAACAC	G	T	Gly	Gly	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to SWISSPROT-ACC:P30044 PUTATIVE PEROXISOMAL ANTIOXIDANT ENZYME (LIVER TISSUE 2D-PAGE SPOT 71B) - Homo sapiens (Human), 161 aa.	1.70E-80	
898	cg43969140	605	CCTCAGCCTGCT CCACAAACCCTG G[C/G]AGGTGTG TCTTGGAACATC CAGGGG	C	G	Leu	Leu	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to SWISSPROT-ACC:P30044 PUTATIVE PEROXISOMAL ANTIOXIDANT ENZYME (LIVER TISSUE 2D-PAGE SPOT 71B) - Homo sapiens (Human), 161 aa.	1.70E-80	
899	cg44024149	417	ATTTCCACAGAA TGATCAAGTTGA C[G/C]ACAGGAA AGGAAGCCGCA CTCAGTT	G	C	Thr	Thr	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to SWISSPROT-ACC:P14555 PHOSPHOLIPASE A2, MEMBRANE ASSOCIATED PRECURSOR (EC 3.1.1.4) (PHOSPHATIDYLCHOLINE 2-ACYLHYDROLASE) (GROUP II PHOSPHOLIPASE A2) - Homo sapiens (Human), 144 aa.	5.30E-79	1 (1p35)
900	cg44024149	453	AAGCCGCACTCA GTTATGGCTTCT A[C/T]GGCTGCC ACTGTGGCGTG GGTGGCA	C	T	Tyr	Tyr	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to SWISSPROT-ACC:P14555 PHOSPHOLIPASE A2, MEMBRANE ASSOCIATED PRECURSOR (EC 3.1.1.4) (PHOSPHATIDYLCHOLINE 2-ACYLHYDROLASE) (GROUP II PHOSPHOLIPASE A2) - Homo sapiens (Human), 144 aa.	5.30E-79	1 (1p35)

901	cg43969316	338	GCTCGAGCTACA GTGGACTACTTG A[G/A]CGACATCA TATTCACACCAA AAATG	G	A	Glu	Glu	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to TREMBLNEW-ACC:CAA19455 Y17G7B.10A PROTEIN CAENORHABDITIS ELEGANS, 514 aa.	7.50E-79	5
902	cg43969316	371	ATATTCACACCA AAAATGTAGAAC A[C/T]ATAATTGA TAGTTTACGGGA TGAAG	C	T	His	His	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to TREMBLNEW-ACC:CAA19455 Y17G7B.10A PROTEIN CAENORHABDITIS ELEGANS, 514 aa.	7.50E-79	5
903	cg43969316	374	TTCACACCAAAA ATGTAGAACACA T[A/T]ATTGATAG TTTACGGGATGA AGGGA	A	T	Ile	Ile	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to TREMBLNEW-ACC:CAA19455 Y17G7B.10A PROTEIN CAENORHABDITIS ELEGANS, 514 aa.	7.50E-79	5
904	cg43969316	377	ACACCAAAAATG TAGAACACATAA T[T/A]GATAGTTT ACGGGATGAAG GGATTG	T	A	Ile	Ile	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to TREMBLNEW-ACC:CAA19455 Y17G7B.10A PROTEIN CAENORHABDITIS ELEGANS, 514 aa.	7.50E-79	5
905	cg43969316	443	AGCGGAGGGAG TACGATGAAGAG AC[A/T]GTTCGAT GGGCAGACGCT GTCATAG	A	T	Thr	Thr	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to TREMBLNEW-ACC:CAA19455 Y17G7B.10A PROTEIN CAENORHABDITIS ELEGANS, 514 aa.	7.50E-79	5
906	cg43969316	458	ATGAAGAGACAG TTCGATGGGCAG A[C/T]GCTGTCAT AGCTGCGGGAG GTGATG	C	T	Asp	Asp	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to TREMBLNEW-ACC:CAA19455 Y17G7B.10A PROTEIN CAENORHABDITIS ELEGANS, 514 aa.	7.50E-79	5
907	cg43327305	199	CACCTGCCTTAA AATTTAAGGTTG A[A/G]AATTTCTT CTGTATGGGATC CCCAT	A	G	Glu	Glu	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to SPTREMBL-ACC:O46606 PHOSPHATIDIC ACID-PREFERRING PHOSPHOLIPASE A1 - BOS TAURUS (BOVINE), 875 aa.	6.10E-78	

908	cg43973026	689	ACAAGGTACTAG CTATGACCAACC G[A/G]AACTTGTC ACCCAAGTCTAC AGGGT	A	G	Phe	Phe	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to SWISSPROT-ACC:P52434 DNA-DIRECTED RNA POLYMERASES I, II, AND III 17.1 KD POLYPEPTIDE (EC 2.7.7.6) (RPB17) (RPB8) - Homo sapiens (Human), 150 aa.	1.00E-75	15
909	cg43931888	295	CCTGGCCACCC CAACGCCGAACT GC[C/G]TCCAGG GAGGCCCACCT GGGAACCC	C	G	Ala	Ala	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to SPTREMBL-ACC:Q16192 ORF3 5' OF PD-ECGF/TP - HOMO SAPIENS (HUMAN), 157 aa.	1.00E-75	22
910	cg42897014	515	TGCGCTCCTGCG GCCGGGCCCGG GC[G/A]TCGCGT GGCAGCGCCAG GAGGCAGA	G	A	Asp	Asp	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to SWISSPROT-ACC:Q15828 CYSTATIN M PRECURSOR (CYSTATIN E) - Homo sapiens (Human), 149 aa.	1.70E-75	11 (11q13)
911	cg43155233	81	AGGATGCATTAA ATACAACTGAGA A[C/T]AAATTGCT TGATGCATATAC TCAGA	C	T	Asn	Asn	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to TREMBLNEW-ACC:CAB46427 HYPOTHETICAL 88.2 KD PROTEIN - HOMO SAPIENS (HUMAN), 785 aa (fragment).	5.60E-75	
912	cg44012742	226	CCCCCATCCAGA ACATCTCATCCA A[T/C]GTGCTAGA GGAGTCCGCCAT CTCCG	T	C	Asn	Asn	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to SPTREMBL-ACC:Q20487 SIMILAR TO RAT TRG GENE PRODUCT. NCBI GI: 1109880 - CAENORHABDITIS ELEGANS, 2018 aa.	1.80E-74	
913	cg36728314	198	TTGGAGTGTTGG CAGTGGGAGGG AC[G/A]TCGATCC GAAGCTCTTTCT GGCTGG	G	A	Asp	Asp	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to TREMBLNEW-ACC:BAA83051 KIAA1099 PROTEIN - HOMO SAPIENS (HUMAN), 804 aa.	1.30E-73	
914	cg43932428	588	CAATGGCCCGCT CGATTTTGCCAA G[C/A]ACCTGGTT ATTGGGTATGGC CCGTC	C	A	Val	Val	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to SPTREMBL-ACC:O60869 EDF-1 PROTEIN - HOMO SAPIENS (HUMAN), 148 aa.	2.50E-72	

915	cg43934599	837	AGAGGGAAAAAG CCAGCAAGACCC A[G/A]AAGCTTTT CCATAGGCTTAG AGAGG	G	A	Leu	Leu	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to TREMBLNEW-ACC:AAD34127 CGI-132 PROTEIN - HOMO SAPIENS (HUMAN), 137 aa.	3.70E-71	10
916	cg43045396	269	AGGAGCAAGCC AGCTGCCTTCAC T[C/T]CGGACAT AAATTCTGGTGC AGACCA	T	C	Arg	Arg	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to SWISSPROT-ACC:P29762 RETINOIC ACID-BINDING PROTEIN I, CELLULAR (CRABP-I) - Homo sapiens (Human), 136 aa.	4.20E-70	15
917	cg43045396	386	GGCCGTCCCCTT CAAGAAGAGTTT G[C/G]GTGCAGT GGATCTTGTTCT CATTCT	C	G	Thr	Thr	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to SWISSPROT-ACC:P29762 RETINOIC ACID-BINDING PROTEIN I, CELLULAR (CRABP-I) - Homo sapiens (Human), 136 aa.	4.20E-70	15
918	cg43045396	503	TGAAGTTGATCT CAGTGGTGCGC AC[C/G]GTGGTG GATGTCTTGATG TAGAACT	C	G	Thr	Thr	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to SWISSPROT-ACC:P29762 RETINOIC ACID-BINDING PROTEIN I, CELLULAR (CRABP-I) - Homo sapiens (Human), 136 aa.	4.20E-70	15
919	cg43045396	617	GCATGGCGTTCA CACCCAGTGCCT T[C/G]AGCAGCT CGTCGAAATTCT CGCTGC	C	G	Leu	Leu	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to SWISSPROT-ACC:P29762 RETINOIC ACID-BINDING PROTEIN I, CELLULAR (CRABP-I) - Homo sapiens (Human), 136 aa.	4.20E-70	15
920	cg42696021	431	GCTTCACACAGT GGCTGTGCCGC CT[T/G]CACAATG AAGTGAACCGGA AGCTGG	T	G	Leu	Leu	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to SWISSPROT-ACC:P55789 AUGMENTER OF LIVER REGENERATION (HERV1 PROTEIN) - Homo sapiens (Human), 125 aa.	1.40E-69	
921	cg42696021	449	GCCGCCTTCACA ATGAAGTGAACC G[G/C]AAGCTGG GCAAGCCTGATT TTGACT	G	C	Arg	Arg	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to SWISSPROT-ACC:P55789 AUGMENTER OF LIVER REGENERATION (HERV1 PROTEIN) - Homo sapiens (Human), 125 aa.	1.40E-69	

922	cg42696021	467	TGAACCGGAAGCTGGGCAAGCCTGA[T/C]TTTGACTGCTCAAGAGTTGATGAGC	T	C	Asp	Asp	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to SWISSPROT-ACC:P55789 AUGMENTER OF LIVER REGENERATION (HERV1 PROTEIN) - Homo sapiens (Human), 125 aa.	1.40E-69	
923	cg42696021	470	ACCGGAAGCTGGGCAAGCCTGATTT[T/C]GACTGCTCAAGAGTTGATGAGCGAT	T	C	Phe	Phe	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to SWISSPROT-ACC:P55789 AUGMENTER OF LIVER REGENERATION (HERV1 PROTEIN) - Homo sapiens (Human), 125 aa.	1.40E-69	
924	cg42696021	485	AGCCTGATTTTGACTGCTCAAGAGT[T/G]GATGAGCGATGGCGTGACGGCTGGA	T	G	Val	Val	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to SWISSPROT-ACC:P55789 AUGMENTER OF LIVER REGENERATION (HERV1 PROTEIN) - Homo sapiens (Human), 125 aa.	1.40E-69	
925	cg42696021	494	TTGACTGCTCAAGAGTTGATGAGC[A/C]TGGCGTGACGGCTGGAAGGACGGCT	A	C	Arg	Arg	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to SWISSPROT-ACC:P55789 AUGMENTER OF LIVER REGENERATION (HERV1 PROTEIN) - Homo sapiens (Human), 125 aa.	1.40E-69	
926	cg42696021	500	GCTCAAGAGTTGATGAGCGATGGC[T/C]GACGGCTGGAAGGACGGCTCCTGTG	T	C	Arg	Arg	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to SWISSPROT-ACC:P55789 AUGMENTER OF LIVER REGENERATION (HERV1 PROTEIN) - Homo sapiens (Human), 125 aa.	1.40E-69	
927	cg42921698	532	AGACCACCTCCGACGTGTCCAGCCG[G/T]GGTTGAAATGCAGGGCGGCATCGG	G	T	Pro	Pro	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to SWISSPROT-ACC:P47929 GALECTIN-7 (HKL-14) - Homo sapiens (Human), 135 aa.	2.30E-69	19
928	cg42921698	547	TGTCCAGCCGGGGGTTGAAATGCAG[G/C]GCGGCATCGGAGCCCCTGCTCCTCCC	G	C	Ala	Ala	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to SWISSPROT-ACC:P47929 GALECTIN-7 (HKL-14) - Homo sapiens (Human), 135 aa.	2.30E-69	19

929	cg42921698	664	TGCCAGGGCGG ATGCCCTCGGG CAG[C/T]GAGGA CTTGTGGGGGA CGTTGGACA	C	T	Ser	Ser	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to SWISSPROT-ACC:P47929 GALECTIN-7 (HKL-14) - Homo sapiens (Human), 135 aa.	2.30E-69	19
930	cg42721336	1100	CCAGCTCCTGTG CTGGCCTCTTCA T[C/T]GCCTCACA CATCGGCTTCGA CTGGC	C	T	Ile	Ile	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to SWISSPROT-ACC:P34629 PUTATIVE AMINOPEPTIDASE ZK353.6 IN CHROMOSOME III (EC 3.4.11.-) - Caenorhabditis elegans, 491 aa.	3.30E-69	
931	cg43930848	573	TACGGGCGCGC GTGCGCACTCC GCA[A/G]CGCGT TCAGGACCCCG GCGCGGGCA	A	G	Leu	Leu	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to SPTREMBL-ACC:O75817 RIBONUCLEASE P PROTEIN SUBUNIT P20 - HOMO SAPIENS (HUMAN), 140 aa.	7.90E-69	7 (7q21)
932	cg43323149	526	GCCTGACTAGTG TGCTGAGCACCA G[C/T]GGAAGCC CTACAGACGGAC TCAGCG	C	T	Ser	Ser	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to SWISSPROT-ACC:P50636 GAMETOGENESIS EXPRESSED PROTEIN GEG-154 - Mus musculus (Mouse), 429 aa.	1.00E-68	1
933	cg43323149	541	TGAGCACCAGC GGAAGCCCTACA GA[C/T]GGACTCA GCGTCATGCAAG GGCCCT	C	T	Asp	Asp	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to SWISSPROT-ACC:P50636 GAMETOGENESIS EXPRESSED PROTEIN GEG-154 - Mus musculus (Mouse), 429 aa.	1.00E-68	1
934	cg43323149	547	CCAGCGGAAGC CCTACAGACGGA CT[C/T]AGCGTCA TGCAAGGGCCCT ACAGCG	C	T	Leu	Leu	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to SWISSPROT-ACC:P50636 GAMETOGENESIS EXPRESSED PROTEIN GEG-154 - Mus musculus (Mouse), 429 aa.	1.00E-68	1
935	cg43323149	550	GCGGAAGCCCT ACAGACGGACTC AG[C/T]GTCATGC AAGGGCCCTACA GCGAAA	C	T	Ser	Ser	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to SWISSPROT-ACC:P50636 GAMETOGENESIS EXPRESSED PROTEIN GEG-154 - Mus musculus (Mouse), 429 aa.	1.00E-68	1

936	cg43323149	553	GAAGCCCTACAG ACGGACTCAGC GT[C/T]ATGCAAG GGCCCTACAGC GAAACAG	C	T	Val	Val	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to SWISSPROT-ACC:P50636 GAMETOGENESIS EXPRESSED PROTEIN GEG-154 - Mus musculus (Mouse), 429 aa.	1.00E-68	1
937	cg43323149	577	TCATGCAAGGGC CCTACAGCGAAA C[A/G]GCCAGCT TTGCTGCCCTTT CAGGGG	A	G	Thr	Thr	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to SWISSPROT-ACC:P50636 GAMETOGENESIS EXPRESSED PROTEIN GEG-154 - Mus musculus (Mouse), 429 aa.	1.00E-68	1
938	cg43323149	589	CCTACAGCGAAA CAGCCAGCTTTG C[T/A]GCCCTTTC AGGGGGCACAC TGAGTG	T	A	Ala	Ala	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to SWISSPROT-ACC:P50636 GAMETOGENESIS EXPRESSED PROTEIN GEG-154 - Mus musculus (Mouse), 429 aa.	1.00E-68	1
939	cg43323149	595	GCGAAACAGCCA GCTTTGCTGCCC T[T/C]TCAGGGG GCACACTGAGTG GTGGCA	T	C	Leu	Leu	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to SWISSPROT-ACC:P50636 GAMETOGENESIS EXPRESSED PROTEIN GEG-154 - Mus musculus (Mouse), 429 aa.	1.00E-68	1
940	cg43323149	607	GCTTTGCTGCCC TTTCAGGGGGCA C[A/G]CTGAGTG GTGGCATTCTCT CCAGTG	A	G	Thr	Thr	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to SWISSPROT-ACC:P50636 GAMETOGENESIS EXPRESSED PROTEIN GEG-154 - Mus musculus (Mouse), 429 aa.	1.00E-68	1
941	cg43323149	616	CCCTTTCAGGGG GCACACTGAGTG G[T/C]GGCATTCT CTCCAGTGGCAA GGGAA	T	C	Gly	Gly	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to SWISSPROT-ACC:P50636 GAMETOGENESIS EXPRESSED PROTEIN GEG-154 - Mus musculus (Mouse), 429 aa.	1.00E-68	1
942	cg43323149	646	TTCTCTCCAGTG GCAAGGGAAAAT A[C/T]AGCCGGTT AGAAGTTCAAGC CGATG	C	T	Tyr	Tyr	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to SWISSPROT-ACC:P50636 GAMETOGENESIS EXPRESSED PROTEIN GEG-154 - Mus musculus (Mouse), 429 aa.	1.00E-68	1

943	cg43323149	650	CTCCAGTGGCAA GGGAAAATACAG C[C/A]GGTTAGAA GTTCAAGCCGAT GTCCA	C	A	Arg	Arg	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to SWISSPROT-ACC:P50636 GAMETOGENESIS EXPRESSED PROTEIN GEG-154 - Mus musculus (Mouse), 429 aa.	1.00E-68	1
944	cg42017985	338	ACAATCTATGCA GTGAAAGAGCTT A[C/T]GATCCTAA GCACTTCCATAA TAGGG	C	T	Tyr	Tyr	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to SWISSNEW-ACC:P56180 PUTATIVE PROTEIN-TYROSINE PHOSPHATASE TPTE (EC 3.1.3.48) - Homo sapiens (Human), 551 aa.	1.80E-68	
945	cg43942922	234	CCACATCTCAGG CCACTAGGGGC AG[A/G]ACAAATA GGTCCTCTGTCA AGACCC	A	G	Arg	Arg	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to SPTREMBL-ACC:Q14676 KIAA0170 PROTEIN - HOMO SAPIENS (HUMAN), 2089 aa.	2.30E-68	
946	cg43942922	345	TCACCTCTGAGC CCACATCTCAGG C[C/T]ACTAGGG GAAGAAAAAATA GGTCCT	C	T	Ala	Ala	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to SPTREMBL-ACC:Q14676 KIAA0170 PROTEIN - HOMO SAPIENS (HUMAN), 2089 aa.	2.30E-68	
947	cg43942922	366	AGGCCACTAGG GGAAGAAAAAAT AG[G/A]TCCTCTG TCAAGACCCCTG AAACAG	G	A	Arg	Arg	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to SPTREMBL-ACC:Q14676 KIAA0170 PROTEIN - HOMO SAPIENS (HUMAN), 2089 aa.	2.30E-68	
948	cg43271511	252	ATGACGGCACTG TCAGAAAGGAAT C[C/T]GGCATTCC GTCAGGCAAATT TGAGG	C	T	Ser	Ser	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to TREMBLNEW-ACC:AAD15557 T-CELL RECEPTOR GAMMA CHAIN, TRGV9 - HOMO SAPIENS (HUMAN), 137 aa.	3.40E-68	7 (7p15)
949	cg42831353	788	GCACCGCGGCG GTGGTGAGGAC ACA[G/A]GCTGC GGTGTAAGCCC GCGTCACCG	G	A	Ala	Ala	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to TREMBLNEW-ACC:AAD37863 PUTATIVE NADH OXIDOREDUCTASE COMPLEX I SUBUNIT - CAENORHABDITIS ELEGANS, 237 aa.	1.30E-67	22

950	cg43973869	385	TGGCGGCACAA CTGCGGCTGATA CC[C/T]TGGGTG GAAAAGATCAGA ATGACAG	C	T	Gln	Gln	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to TREMBLNEW-ACC:AAD36983 MAP KINASE PHOSPHATASE-LIKE PROTEIN MK-STYX - HOMO SAPIENS (HUMAN), 313 aa.	3.10E-67	7
951	cg43999983	413	CTTCCAAATTAG CTTCAGTTTTCA G[T/A]GAGCAAC CATTAAATCCTAT ATAAA	T	A	Ser	Ser	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to TREMBLNEW-ACC:CAB43446 HYPOTHETICAL 34.0 KD PROTEIN - ARABIDOPSIS THALIANA (MOUSE-EAR CRESS), 299 aa.	1.00E-66	
952	cg43080742	266	AGACGGTGGCC TCGCTGTGGCC GGC[G/C]CTGCA GGAACTGGCCC GGTGTGGGA	G	C	Ala	Ala	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to SWISSNEW-ACC:P53603 FORMIMINOTRANSFERASE-CYCLODEAMINASE (FTCD) [INCLUDES: GLUTAMATE FORMIMINOTRANSFERASE (EC 2.1.2.5) (GLUTAMATE FORMYLTRANSFERASE) FORMIMINOTETRAHYDROFOLATE CYCLODEAMINASE (EC 4.3.1.4)] - Sus scrofa (Pig), 541 aa.	2.20E-66	21
953	cg43927424	304	CGCAGTATTTCA GAGAAAAGTATA C[T/A]CTTCAGCT GAAGTACCCGCA CCTTC	T	A	Thr	Thr	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to SPTREMBL-ACC:O77503 TRANSLATION INITIATION FACTOR EIF2C - ORYCTOLAGUS CUNICULUS (RABBIT), 813 aa.	1.90E-65	
954	cg43919145	1731	CCTCAACAGACT GCCTTTGTTCAC T[G/A]TCTGGAGA AGATAGCAAAGG AGTAG	G	A	Asp	Asp	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to TREMBLNEW-ACC:CAB52430 DJ703H14.1 PROTEIN - HOMO SAPIENS (HUMAN), 485 aa (fragment).	3.20E-65	1
955	cg42381630	261	CGACCTATTATT GGCCTAGACCAA G[G/A]CGCTATGT ACAGCCTCCTGA AATGA	G	A	Arg	Arg	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to SPTREMBL-ACC:O76087 GAGE-8 - HOMO SAPIENS (HUMAN), 117 aa.	5.90E-64	

956	cg42381630	267	ATTATTGGCCTAGACCAAGGCGCTA[T/C]GTACAGCCTCCTGAAATGATTGGGC	T	C	Tyr	Tyr	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to SPTREMBL-ACC:O76087 GAGE-8 - HOMO SAPIENS (HUMAN), 117 aa.	5.90E-64	
957	cg43132517	529	TCCATCTTCAGACACCCCCCCGTCT[C/T]TCTGCACAGGGAGTTGGCCTTCCAG	C	T	Glu	Glu	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to SPTREMBL-ACC:Q12799 T-COMPLEX PROTEIN 10A - HOMO SAPIENS (HUMAN), 416 aa.	2.60E-63	
958	cg43132517	556	CTGCACAGGGAGTTGGCCTTCCAGT[A/G]GGTGTTGCTCTTCTGTCTTGACGTC	A	G	Pro	Pro	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to SPTREMBL-ACC:Q12799 T-COMPLEX PROTEIN 10A - HOMO SAPIENS (HUMAN), 416 aa.	2.60E-63	
959	cg43950549	237	AGAAACCGGATGATGCACAGTATTA[C/T]TGTCAAAGAGCTTATTGTCACATTC	C	T	Tyr	Tyr	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to TREMBLNEW-ACC:AAD30062 SUPPRESSOR OF G2 ALLELE OF SKP1 HOMOLOG - HOMO SAPIENS (HUMAN), 333 aa.	1.40E-62	
960	cg43950549	432	GACAAAAATTAGATAGTGCAGATAC[C/T]AATTTCAGTGACTGGATTAAAAGGT	C	T	Thr	Thr	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to TREMBLNEW-ACC:AAD30062 SUPPRESSOR OF G2 ALLELE OF SKP1 HOMOLOG - HOMO SAPIENS (HUMAN), 333 aa.	1.40E-62	
961	cg43969918	863	TTGCGGCCACTTGGGCCTTGAGAAT[G/A]GCAGCTTTTCCTCGGCCAGCCCCTG	G	A	Ala	Ala	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to SWISSPROT-ACC:P43331 SMALL NUCLEAR RIBONUCLEOPROTEIN SM D3 (SNRNP CORE PROTEIN D3) (SM-D3) - Homo sapiens (Human), 126 aa.	2.90E-62	22
962	cg43950850	526	CCGTCGCGATCGGCCTCCGCCGGAT[C/T]AGGTTATCAATCAGGCCGGAGCAGT	C	T	Leu	Leu	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to SWISSNEW-ACC:O95298 NADH-UBIQUINONE OXIDOREDUCTASE SUBUNIT B14.5B (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-B14.5B) (CI-B14.5B) - Homo sapiens (Human), 119 aa.	7.80E-62	11

963	cg42672206	593	GCCCTGAGACCACTAAACCTTGATT[T/C]TTTACAGGCTCAGAGACCATGGAAC	T	C	Lys	Lys	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to SPTREMBL-ACC:O55129 MICROTUBULE-ASSOCIATED PROTEIN 6 (STOP PROTEIN) - MUS MUSCULUS (MOUSE), 906 aa.	1.30E-61	
964	cg44926530	1939	CTGCACAGGTCACAATATATTTATA[G/A]GCTTTTCCCAACTTAACCAGGTGTG	G	A	Ala	Ala	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to SWISSPROT-ACC:P51808 PROTEIN 91/23 - Homo sapiens (Human), 116 aa.	2.10E-61	X
965	cg43918476	2024	TGAGCATGACCCGATCTTGAACTTC[A/G]CTGTACTGCAGGTTAACTACCTTGT	A	G	Ser	Ser	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to TREMBLNEW-ACC:AAD34122 CGI-127 PROTEIN - HOMO SAPIENS (HUMAN), 121 aa.	6.30E-61	2
966	cg43285334	682	CGGTGACCCGGGCGTCAGTGTCCCC[G/A]TAACCAGAGTAGGCCAGCAGTGATC	G	A	Tyr	Tyr	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to TREMBLNEW-ACC:AAD20965 HSPC003 - HOMO SAPIENS (HUMAN), 125 aa.	1.90E-60	1
967	cg42313635	272	GGGTGAGCAGCAAACAGGAGGTGAC[A/G]CAGATTCCTGCAGCTCTGAGTGTCC	A	G	Thr	Thr	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to REMTREMBL-ACC:G598237 T CELL RECEPTOR ALPHA CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 134 aa (fragment).	8.00E-60	
968	cg43985327	429	TCGCGCAGGCCAGACAGCGGTGCAG[A/G]CCGCCCCCTGGCAGGTCGGGGTCGA	A	G	Gly	Gly	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to SPTREMBL-ACC:O00488 ZINC FINGER PROTEIN - HOMO SAPIENS (HUMAN), 116 aa.	2.10E-59	1
969	cg43939569	691	GCATCCTCAGCTCGGAGATGAATTC[G/T]CTTCCGGATCAAGAAGTAGAACTGA	G	T	Arg	Arg	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to TREMBLNEW-ACC:AAD32455 GANGLIOSIDE EXPRESSION FACTOR 2 HOMOLOG - HOMO SAPIENS (HUMAN), 117 aa.	3.50E-59	17

970	cg43924537	521	ATCCATTGGCTTTATCCACAGCCTG[C/A]AGGACTCGCTGGATGCTCTCCTTGT	C	A	Leu	Leu	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to SPTREMBL-ACC:Q08726 CHROMOSOME XV READING FRAME ORF YOR262W - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 347 aa.	1.20E-58	
971	cg43920127	340	AAAGATGCAGTTCATAATGTTCTCC[C/A]GATTCAGGAACTCTTATGCTGTGTC	C	A	Ser	Ser	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to SPTREMBL-ACC:O75273 R26984_1 - HOMO SAPIENS (HUMAN), 508 aa (fragment).	3.10E-58	15
972	cg40968986	217	CGCGCCTCCTGCTGGCTGCACTGGT[G/C]CAGGACTATGTGCAGATGAAGGCCA	G	C	Val	Val	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to SWISSNEW-ACC:P06881 CALCITONIN GENE-RELATED PEPTIDE I PRECURSOR (CGRP-I) (ALPHA-TYPE CGRP) - Homo sapiens (Human), 128 aa.	5.10E-58	11 (11p15.2)
973	cg40968986	262	AGGCCAGTGAGCTGGAGCAGGAGCA[A/G]GAGAGAGAGGGCTCCAGAATCATTG	A	G	Gln	Gln	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to SWISSNEW-ACC:P06881 CALCITONIN GENE-RELATED PEPTIDE I PRECURSOR (CGRP-I) (ALPHA-TYPE CGRP) - Homo sapiens (Human), 128 aa.	5.10E-58	11 (11p15.2)
974	cg40968986	304	GAATCATTGCCCAGAAGAGAGCCTG[T/C]GACACTGCCACCTGTGTGACTCATC	T	C	Cys	Cys	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to SWISSNEW-ACC:P06881 CALCITONIN GENE-RELATED PEPTIDE I PRECURSOR (CGRP-I) (ALPHA-TYPE CGRP) - Homo sapiens (Human), 128 aa.	5.10E-58	11 (11p15.2)
975	cg40968986	361	CAGGCTTGCTGAGCAGATCAGGGGG[T/C]GTGGTGAAGAACAACTTTGTGCCCA	T	C	Gly	Gly	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to SWISSNEW-ACC:P06881 CALCITONIN GENE-RELATED PEPTIDE I PRECURSOR (CGRP-I) (ALPHA-TYPE CGRP) - Homo sapiens (Human), 128 aa.	5.10E-58	11 (11p15.2)
976	cg40968986	379	CAGGGGGTGTGGTGAAGAACAACTT[T/C]GTGCCCACCAATGTGGGTTCCAAAG	T	C	Phe	Phe	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to SWISSNEW-ACC:P06881 CALCITONIN GENE-RELATED PEPTIDE I PRECURSOR (CGRP-I) (ALPHA-TYPE CGRP) - Homo sapiens (Human), 128 aa.	5.10E-58	11 (11p15.2)

977	cg42165615	217	GGATCCTGGCCT CGGAGAAGCGG TC[A/G]TAGAAAG GAGAGCGCAAC AGGTAGT	A	G	Tyr	Tyr	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to TREMBLNEW-ACC:AAD22466 PEROXISOMAL BIOGENESIS FACTOR 16 - HOMO SAPIENS (HUMAN), 336 aa.	3.50E-57	
978	cg43052776	294	AGGGTGGGAGA TTCCTGATGGGA AC[G/A]AATTCTC CAGACAGCAGA GATGGTG	G	A	Thr	Thr	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to TREMBLNEW-ACC:CAB43247 HYPOTHETICAL 34.8 KD PROTEIN - HOMO SAPIENS (HUMAN), 323 aa (fragment).	3.60E-57	
979	cg43999272	459	AGAAGGCGGTG ACTCCAGCTCCT CC[C/T]ATAAAGA GGTGGGAGCTG TCCTCGG	C	T	Pro	Pro	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to TREMBLNEW-ACC:AAD05427 NADH-UBIQUINONE OXIDOREDUCTASE B14.5A SUBUNIT - HOMO SAPIENS (HUMAN), 113 aa.	3.20E-56	19
980	cg43300763	922	CTCGGCGAAGG AGCATCTTTGAA TA[C/T]CACCGCA TAGAGCTGGACC CCAGCA	C	T	Tyr	Tyr	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to SPTREMBL-ACC:Q18500 HYPOTHETICAL PROTEIN C36E8.3 - CAENORHABDITIS ELEGANS, 476 aa.	3.20E-56	
981	cg43319008	251	TTAAATTATATAG CAGCATCACCAA [C/T]CAACAGAG GAGATACCTTGA GAAGC	C	T	Asn	Asn	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to TREMBLNEW-ACC:BAA20786 KIAA0328 PROTEIN - HOMO SAPIENS (HUMAN), 1661 aa (fragment).	9.20E-56	2
982	cg43969932	1229	CGTTCTGCACCG TCTCCTTCCGAG C[A/G]TTGAATTT CTTCCCCTTGTA GATGT	A	G	Asn	Asn	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to SPTREMBL-ACC:Q20124 SIMILAR TO S. CEREVISIAE YJU2 PROTEIN - CAENORHABDITIS ELEGANS, 323 aa.	1.10E-55	
983	cg43935092	99	TGGAGCGGTGC CAGCAGCAGGC GAA[C/T]GAGGT GACGGAAATTAT GCGTAACA	C	T	Asn	Asn	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to TREMBLNEW-ACC:AAD26992 VAMP5-LIKE PROTEIN HOMO SAPIENS (HUMAN), 116 aa.	1.80E-55	2

984	cg43942680	699	CGGAGGAGAGC GCCCTCAATCAC GT[G/C]CAGCAC CCGAGCGACGA AGCCGAGG	G	C	Val	Val	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to TREMBLNEW-ACC:AAD38498 T-CELL ACTIVATION PROTEIN - HOMO SAPIENS (HUMAN), 127 aa.	1.80E-55	10
985	cg43269198	536	GCTGGCAGTCTA CCACGCTGATTT G[G/A]AACTCGCT GGAAGGCAACAT TTCAA	G	A	Phe	Phe	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to TREMBLNEW-ACC:CAB41301 DJ596C15.1.1 (NOVEL PROTEIN) (ISOFORM 1) - HOMO SAPIENS (HUMAN), 162 aa (fragment).	1.80E-55	20
986	cg43917388	701	GGATGTCCACAT TGACCACGTGCA C[A/G]GGCTGGC AGGTCTCCTGTT CTCTGG	A	G	Pro	Pro	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to SPTREMBL-ACC:Q22453 SIMILARTO LDL RECEPTOR-RELATED PROTEIN. NCBI GI: 1055166 - CAENORHABDITIS ELEGANS, 1357 aa.	2.30E-55	1
987	cg43917989	775	TGGGCATGCTTG CTGGGGCCGCC AC[G/T]GGTGCT GCTCTTGGCTCA CTTATGT	G	T	Thr	Thr	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to TREMBLNEW-ACC:AAD23762 EVECTIN-1 - RATTUS NORVEGICUS (RAT), 223 aa.	2.30E-55	11
988	cg43917989	793	CCGCCACGGGT GCTGCTCTTGGC TC[A/G]CTTATGT GGTCGCCTTGCT GGTTCT	A	G	Ser	Ser	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to TREMBLNEW-ACC:AAD23762 EVECTIN-1 - RATTUS NORVEGICUS (RAT), 223 aa.	2.30E-55	11
989	cg43917989	796	CCACGGGTGCT GCTCTTGGCTCA CT[T/C]ATGTGGT CGCCTTGCTGGT TCTGAG	T	C	Leu	Leu	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to TREMBLNEW-ACC:AAD23762 EVECTIN-1 - RATTUS NORVEGICUS (RAT), 223 aa.	2.30E-55	11
990	cg43917989	808	CTCTTGGCTCAC TTATGTGGTCGC C[T/C]TGCTGGTT CTGAGCCCTGG GGCTCG	T	C	Pro	Pro	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to TREMBLNEW-ACC:AAD23762 EVECTIN-1 - RATTUS NORVEGICUS (RAT), 223 aa.	2.30E-55	11

991	cg41664708	357	AGCAATCGACCAATACAGCTGTGAC[C/T]CTGACTGGCTAGTAGTCTCTGGCAC	C	T	Thr	Thr	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to SWISSNEW-ACC:P47992 LYMPHOTACTIN PRECURSOR (CYTOKINE SCM-1) (ATAC) (LYMPHOTAXIN) (SCM-1-ALPHA) - Homo sapiens (Human), 114 aa.	2.00E-54	1
992	cg43332460	324	GGAACATCTGCGTCAGCTCCGTGTC[T/C]CCAAACTCCTGGGGGAGGTGGTAGA	T	C	Gly	Gly	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to SPTREMBL-ACC:Q91579 RIBONUCLEOPROTEIN - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 462 aa.	5.40E-54	
993	cg42855650	520	CCGGGCCCCTCATAGGAGAGGAAGC[T/C]CGGGAGGTGGCCAGGCGGCAGGAAG	T	C	Ala	Ala	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to SWISSNEW-ACC:O00230 CORTISTATIN PRECURSOR [CONTAINS: CORTISTATIN-29; CORTISTATIN-17] - Homo sapiens (Human), 105 aa.	7.90E-53	
994	cg42903443	49	TCACCGCCAGGAGGACGCATTCGGC[G/C]GAACCCAGAGCCAGCGATGCGCACA	G	C	Ser	Ser	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to TREMBLNEW-ACC:CAB45012 573K1.15 (MM17M1-6 (NOVEL 7 TRANSMEMBRANE RECEPTOR (RHODOPSIN FAMILY) (OLFACTORY RECEPTOR LIKE) PROTEIN)) - MUS MUSCULUS (MOUSE), 309 aa (fragment).	1.90E-51	
995	cg44027270	229	CAGAGTCCATTACTTTTCTTCTGTT[A/G]AATTTCACTGTTGTTGTCTTTTCTG	A	G	Phe	Phe	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to SPTREMBL-ACC:O14737 TFAR19 - HOMO SAPIENS (HUMAN), 125 aa.	2.20E-50	
996	cg44027270	499	GTTGGGCCGCATCACCAGGATCCTG[T/G]CGGCTAAACTTGGGTCATAACAACT	T	G	Arg	Arg	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to SPTREMBL-ACC:O14737 TFAR19 - HOMO SAPIENS (HUMAN), 125 aa.	2.20E-50	
997	cg41568177	226	CATTCTTGTCCTTTTTCTCAAAGAC[A/G]TCGGCGAGGTAATTTGTGCCCTTTT	A	G	Asp	Asp	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to SWISSNEW-ACC:P31151 S100 CALCIUM-BINDING PROTEIN A7 (PSORIASIN) - Homo sapiens (Human), 100 aa.	4.50E-50	1 (1q21)

998	cg44010855	651	CCTGGAACGAGAAGCGCAGGGTCTA[C/T]GAAGAATAGGGTGAAAAACCTCAGA	C	T	Tyr	Tyr	SILENT-CODING	UNCLASSIFIED	Human Gene Similar to TREMBLNEW-ACC:AAD38944 NJAC PROTEIN - HOMO SAPIENS (HUMAN), 99 aa.	5.80E-50	5
999	cg44917490	446	TCTGGGCTCGGCTGAAGGGGTGAAG[G/A]GGGCCGGGTCAGGGTCGTTCCTCCA	G	A			SILENT-NONCODING	amyloid	Human Gene SWISSPROT-ID:P51693 AMYLOID-LIKE PROTEIN 1 PRECURSOR (APLP) - HOMO SAPIENS (HUMAN), 650 aa.	0.00E+00	19
1000	cg43921977	3515	CAGCCGCGGACCGTAGCTGGCACTA[C/T]CCGCTCCTGCCGCCGCTCCGCCTCA	C	T			SILENT-NONCODING	apoptosis	Human Gene SWISSPROT-ID:P55060 CELLULAR APOPTOSIS SUSCEPTIBILITY PROTEIN - HOMO SAPIENS (HUMAN), 971 aa.	0.00E+00	20
1001	cg43921977	442	GGAATTCGTGACAAGTTCAAAAGGA[G/A]AACTTCCTTTGTTTTAATGCAGCTG	G	A			SILENT-NONCODING	apoptosis	Human Gene SWISSPROT-ID:P55060 CELLULAR APOPTOSIS SUSCEPTIBILITY PROTEIN - HOMO SAPIENS (HUMAN), 971 aa.	0.00E+00	20
1002	cg42840476	5048	TGTAATCCCAGCTCCTTGGGAGGCT[A/G]AGACAGGAGGATTCCTTGAGCCCTG	A	G			SILENT-NONCODING	apoptosis	Human Gene SWISSPROT-ID:O14727 APOPTOTIC PROTEASE ACTIVATING FACTOR 1 (APAF-1) - HOMO SAPIENS (HUMAN), 1194 aa.	0.00E+00	
1003	cg43970780	245	GGCAGGAGATAAACCATCCAGCAGA[T/G]TTTTCTGTGTAAAAACATTTATTTT	T	G			SILENT-NONCODING	apoptosis	Human Gene SWISSNEW-ID:Q92785 ZINC-FINGER PROTEIN UBI-D4 (APOPTOSIS RESPONSE ZINC FINGER PROTEIN REQUIEM) - HOMO SAPIENS (HUMAN), 391 aa.\|pcls:SWISSPROT-ID:Q92785 ZINC-FINGER PROTEIN UBI-D4 (APOPTOSIS RESPONSE ZINC FINGER PROTEIN REQUIEM) - HOMO SAPIENS (HUMAN), 391 aa.	2.30E-212	11

1004	cg44001801	997	AGTAAATATCCC CTTGGCTGTGTT T[T/gap]GTCAA CATTGGGATTCT TTTTGCC	T	gap		SILENT-NONCODING	apoptosis	Human Gene SWISSPROT-ID:P55210 CASPASE-7 PRECURSOR (EC 3.4.22.-) (ICE-LIKE APOPTOTIC PROTEASE 3) (ICE-LAP3) (APOPTOTIC PROTEASE MCH-3) (CMH-1) - HOMO SAPIENS (HUMAN), 303 aa.	6.00E-166	10
1005	cg44001801	1041	TTTTGCCAAGTG CAAACATGACTC T[A/G]CCACTGTT ACCACCAATTGC AGTGG	A	G		SILENT-NONCODING	apoptosis	Human Gene SWISSPROT-ID:P55210 CASPASE-7 PRECURSOR (EC 3.4.22.-) (ICE-LIKE APOPTOTIC PROTEASE 3) (ICE-LAP3) (APOPTOTIC PROTEASE MCH-3) (CMH-1) - HOMO SAPIENS (HUMAN), 303 aa.	6.00E-166	10
1006	cg44001801	1050	GTGCAAACATGA CTCTACCACTGT T[A/G]CCACCAAT TGCAGTGGACAC AGCCA	A	G		SILENT-NONCODING	apoptosis	Human Gene SWISSPROT-ID:P55210 CASPASE-7 PRECURSOR (EC 3.4.22.-) ((ICE-LIKE APOPTOTIC PROTEASE 3) (ICE-LAP3) (APOPTOTIC PROTEASE MCH-3) (CMH-1) - HOMO SAPIENS (HUMAN), 303 aa.	6.00E-166	10
1007	cg44001801	1238	AATTCAGAGAAC AAAAGACAGCAC C[C/gap]AGAAAG TTTCTTCCCTGTT GAATCA	C	gap		SILENT-NONCODING	apoptosis	Human Gene SWISSPROT-ID:P55210 CASPASE-7 PRECURSOR (EC 3.4.22.-) ((ICE-LIKE APOPTOTIC PROTEASE 3) (ICE-LAP3) (APOPTOTIC PROTEASE MCH-3) (CMH-1) - HOMO SAPIENS (HUMAN), 303 aa.	6.00E-166	10
1008	cg44001801	270	TATTTTAAAGCTA TAACAGATTTTG[C/G]ACATAAAGC CAAAACAGATTG TTTT	C	G		SILENT-NONCODING	apoptosis	Human Gene SWISSPROT-ID:P55210 CASPASE-7 PRECURSOR (EC 3.4.22.-) ((ICE-LIKE APOPTOTIC PROTEASE 3) (ICE-LAP3) (APOPTOTIC PROTEASE MCH-3) (CMH-1) - HOMO SAPIENS (HUMAN), 303 aa.	6.00E-166	10

1009	cg44001801	571	CAGCTCACTCCA TCTCAGTCAGTG G[C/T]TTTGTTCT TGTCATGGCTCC ATTTT	C	T		SILENT-NONCODING	apoptosis	Human Gene SWISSPROT-ID:P55210 CASPASE-7 PRECURSOR (EC 3.4.22.-) (ICE-LIKE APOPTOTIC PROTEASE 3) (ICE-LAP3) (APOPTOTIC PROTEASE MCH-3) (CMH-1) - HOMO SAPIENS (HUMAN), 303 aa.	6.00E-166	10
1010	cg44001801	714	AAACCTCTTCCC ATTATCCTCATA G[C/A]CCTGGGT GTGGTAACAGCT TCTTGC	C	A		SILENT-NONCODING	apoptosis	Human Gene SWISSPROT-ID:P55210 CASPASE-7 PRECURSOR (EC 3.4.22.-) (ICE-LIKE APOPTOTIC PROTEASE 3) (ICE-LAP3) (APOPTOTIC PROTEASE MCH-3) (CMH-1) - HOMO SAPIENS (HUMAN), 303 aa.	6.00E-166	10
1011	cg44001801	747	GTGGTAACAGCT TC[T]GCTGTTTG G[C/G]TTCTCTTT TATCATCTATGTA AGTC	C	G		SILENT-NONCODING	apoptosis	Human Gene SWISSPROT-ID:P55210 CASPASE-7 PRECURSOR (EC 3.4.22.-) (ICE-LIKE APOPTOTIC PROTEASE 3) (ICE-LAP3) (APOPTOTIC PROTEASE MCH-3) (CMH-1) - HOMO SAPIENS (HUMAN), 303 aa.	6.00E-166	10
1012	cg44001801	755	AGCTTCTTGCTG TTTGGCTTCTCT T[T/A]TATCATCT ATGTAAGTCAAT TTCCT	T	A		SILENT-NONCODING	apoptosis	Human Gene SWISSPROT-ID:P55210 CASPASE-7 PRECURSOR (EC 3.4.22.-) (ICE-LIKE APOPTOTIC PROTEASE 3) (ICE-LAP3) (APOPTOTIC PROTEASE MCH-3) (CMH-1) - HOMO SAPIENS (HUMAN), 303 aa.	6.00E-166	10
1013	cg43921971	1242	CAGCTGCATTAA AACAAAGGAAGT T[T/C]TCCTTTTG AACTTGTCACGA ATTCC	T	C		SILENT-NONCODING	apoptosis	Human Gene Similar to SWISSPROT-ID:P55060 CELLULAR APOPTOSIS SUSCEPTIBILITY PROTEIN - HOMO SAPIENS (HUMAN), 971 aa.	6.10E-68	
1014	cg43042134	636	TAATAAATTAATT CTAAAGTTTAGA[T/C]GATGTTTTG GTTCTTCTTCAT GAAA	T	C		SILENT-NONCODING	apoptosis inhib	Human Gene SPTREMBL-ID:Q13489 INHIBITOR OF APOPTOSIS PROTEIN 1 - HOMO SAPIENS (HUMAN), 604 aa.	0.00E+00	11

1015	cg43983747	26	TTTTTTTTTTTTTTTTTTTTT[C/T]TCATTAAACTTCTGGGCTTTATTTA	C	T			SILENT-NONCODING	apoptosis inhib	Human Gene Homologous to SWISSPROT-ID:Q92843 APOPTOSIS REGULATOR BCL-W (KIAA0271) - HOMO SAPIENS (HUMAN), 193 aa.	2.1E-101	
1016	cg43983747	28	TTTTTTTTTTTTTTTTTTTTCT[C/T]ATTAAACTTCTGGGCTTTATTTATT	C	T			SILENT-NONCODING	apoptosis inhib	Human Gene Homologous to SWISSPROT-ID:Q92843 APOPTOSIS REGULATOR BCL-W (KIAA0271) - HOMO SAPIENS (HUMAN), 193 aa.	2.1E-101	
1017	cg43324271	2553	CCTGTTAAAAACAAAGTGCAGTCAG[A/T]TTCTAAGCCCTGTTCAGAGACTTCG	A	T			SILENT-NONCODING	apoptosis recep	Human Gene SWISSPROT-ID:Q13546 SERINE/THREONINE PROTEIN KINASE RIP (EC 2.7.1.-) (CELL DEATH PROTEIN RIP) (RECEPTOR INTERACTING PROTEIN) - HOMO SAPIENS (HUMAN), 671 aa.	0	6
1018	cg43917593	306	CAGATAAGCAAGTGAGATCCTCTGG[C/T]CCTTAATCATCAATATACTCAAATG	C	T			SILENT-NONCODING	ATPase_associated	Human Gene SWISSNEW-ID:Q99460 26S PROTEASOME REGULATORY SUBUNIT S1 (P112) - HOMO SAPIENS (HUMAN), 953 aa.	0	2
1019	cg43987714	2968	AGTGACCACCAGGGGCTCTGAACTG[C/T]AGCTGATGTTATCAGCAGGCCATGC	C	T			SILENT-NONCODING	ATPase_associated	Human Gene SWISSNEW-ID:Q13200 26S PROTEASOME REGULATORY SUBUNIT S2 (P97) (TUMOR NECROSIS FACTOR TYPE 1 RECEPTOR ASSOCIATED PROTEIN 2) (55.11 PROTEIN) - HOMO SAPIENS (HUMAN), 909 aa.\|pcls:SWISSPROT-ID:Q13200 26S PROTEASOME REGULATORY SUBUNIT S2 (P97) (TUMOR NECROSIS FACTOR TYPE 1 RECEPTOR ASSOCIATED PROTEIN 2) (55.11 PROTEIN) - HOMO SAPIENS (HUMAN), 909 aa.	0	3

1020	cg43987714	2992	GCAGCTGATGTTATCAGCAGGCCAT[G/gap]CATCCTGCTGCCAAGGGTGGACACG	G	gap			SILENT-NONCODING	ATPase_associated	Human Gene SWISSNEW-ID:Q13200 26S PROTEASOME REGULATORY SUBUNIT S2 (P97) (TUMOR NECROSIS FACTOR TYPE 1 RECEPTOR ASSOCIATED PROTEIN 2) (55.11 PROTEIN) - HOMO SAPIENS (HUMAN), 909 aa.\|pcls:SWISSPROT-ID:Q13200 26S PROTEASOME REGULATORY SUBUNIT S2 (P97) (TUMOR NECROSIS FACTOR TYPE 1 RECEPTOR ASSOCIATED PROTEIN 2) (55.11 PROTEIN) - HOMO SAPIENS (HUMAN), 909 aa.	0	3
1021	cg43924820	1166	CAAATACCTGGATTTTTTTTTTTTT[gap/T]GTACACTGGTTCATAGATCGGCACT	gap	T			SILENT-NONCODING	ATPase_associated	Human Gene SWISSNEW-ID:Q14974 IMPORTIN BETA-1 SUBUNIT (KARYOPHERIN BETA-1 SUBUNIT) (NUCLEAR FACTOR P97) (IMPORTIN 90) - HOMO SAPIENS (HUMAN), 876 aa.\|pcls:SWISSPROT-ID:Q14974 IMPORTIN BETA-1 SUBUNIT (KARYOPHERIN BETA-1 SUBUNIT) (NUCLEAR FACTOR P97) (IMPORTIN 90) - HOMO SAPIENS (HUMAN), 876 aa.\|pcls:SPTREMBL-ID:Q14974 NUCLEAR FACTOR P97 - HOMO SAPIENS (HUMAN), 876 aa.	0	17
1022	cg43944573	820	AGGAGCCACCTTTGCTGGGCTCGGC[C/gap]TCTACCAAGCAGAAATGCGATTACA	C	gap			SILENT-NONCODING	ATPase_associated	Human Gene SPTREMBL-ID:Q99721 TBP-ASSOCIATED FACTOR - HOMO SAPIENS (HUMAN), 947 aa (fragment).	0	20
1023	cg43277630	3793	ATCATGTTTCTGAGACCACAGTTTA[A/C]AACAGGTGTGCCTGTTGCTTTCTTC	A	C			SILENT-NONCODING	ATPase_associated	Human Gene SWISSPROT-ID:P35670 COPPER-TRANSPORTING ATPASE 2 (EC 3.6.1.36) (COPPER PUMP 2) (WILSON DISEASE-ASSOCIATED PROTEIN) - HOMO SAPIENS (HUMAN), 1465 aa.	0	13 (13q14.3)

1024	cg43277630	3794	TCATGTTTCTGAGACCACAGTTTAA[A/C]ACAGGTGTGCCTGTTGCTTTCTTCC	A	C			SILENT-NONCODING	ATPase_associated	Human Gene SWISSPROT-ID:P35670 COPPER-TRANSPORTING ATPASE 2 (EC 3.6.1.36) (COPPER PUMP 2) (WILSON DISEASE-ASSOCIATED PROTEIN) - HOMO SAPIENS (HUMAN), 1465 aa.	0	13 (13q14.3)
1025	cg43277630	4360	TCGTGGGGTTCAGTAGAGAATTCAA[G/T]TGACTAGCGCCTGGCCTTGTGTGGC	G	T			SILENT-NONCODING	ATPase_associated	Human Gene SWISSPROT-ID:P35670 COPPER-TRANSPORTING ATPASE 2 (EC 3.6.1.36) (COPPER PUMP 2) (WILSON DISEASE-ASSOCIATED PROTEIN) - HOMO SAPIENS (HUMAN), 1465 aa.	0	13 (13q14.3)
1026	cg43277630	4504	CCACAGCACCCCGAAGGGAGCATCT[A/G]TTTACCTGGCAGTGGCTCTCAGAGC	A	G			SILENT-NONCODING	ATPase_associated	Human Gene SWISSPROT-ID:P35670 COPPER-TRANSPORTING ATPASE 2 (EC 3.6.1.36) (COPPER PUMP 2) (WILSON DISEASE-ASSOCIATED PROTEIN) - HOMO SAPIENS (HUMAN), 1465 aa.	0	13 (13q14.3)
1027	cg43920091	21	TTTTTTTTTTTTTAGGGGGC[G/A]GGACATGCTTTATTTTCAGCCACAG	G	A			SILENT-NONCODING	ATPase_associated	Human Gene SWISSPROT-ID:Q13608 PEROXISOME ASSEMBLY FACTOR-2 (PAF-2) (PEROXISOMAL-TYPE ATPASE 1) (PEROXIN-6) - HOMO SAPIENS (HUMAN), 980 aa.	0	6 (6p21.1)
1028	cg43247872	1766	GTTGATAACCATATGCACTTAACAT[T/gap]ATATTCTATAAACATTAAGTAGTGC	T	gap			SILENT-NONCODING	ATPase_associated	Human Gene SWISSPROT-ID:P48723 MICROSOMAL STRESS 70 PROTEIN ATPASE CORE PRECURSOR - HOMO SAPIENS (HUMAN), 471 aa.	5.2E-247	21
1029	cg43247872	1802	ACATTAAGTAGTGCCAGTTATGAGA[gap/C]TTCCCAGTTCTTACTAAATTGTATT	gap	C			SILENT-NONCODING	ATPase_associated	Human Gene SWISSPROT-ID:P48723 MICROSOMAL STRESS 70 PROTEIN ATPASE CORE PRECURSOR - HOMO SAPIENS (HUMAN), 471 aa.	5.2E-247	21
1030	cg43247872	1878	TATCACATGTAACTAATAATTTGAA[C/G]TATACTTGAAGGACCGTGTTGATGT	C	G			SILENT-NONCODING	ATPase_associated	Human Gene SWISSPROT-ID:P48723 MICROSOMAL STRESS 70 PROTEIN ATPASE CORE PRECURSOR - HOMO SAPIENS (HUMAN), 471 aa.	5.2E-247	21

1031	cg43247872	1943	GGTTGGAAGATA GCAGTATTATTA G[C/gap]ATAAGC TGCATACGTAAT ATTCAGT	C	gap			SILENT-NONCODING	ATPase_associated	Human Gene SWISSPROT-ID:P48723 MICROSOMAL STRESS 70 PROTEIN ATPASE CORE PRECURSOR - HOMO SAPIENS (HUMAN), 471 aa.	5.2E-247	21
1032	cg43247872	2121	TATTCAAATGTTT CAGCACCATATA[A/G]TAGAAATAC CCAATTATATTCT AGT	A	G			SILENT-NONCODING	ATPase_associated	Human Gene SWISSPROT-ID:P48723 MICROSOMAL STRESS 70 PROTEIN ATPASE CORE PRECURSOR - HOMO SAPIENS (HUMAN), 471 aa.	5.2E-247	21
1033	cg43958825	101	CGTGAGACTGG GGCTGGCCTGT GTG[C/gap]CCTA GGCGTAGTATTG TAGGTTGGC	C	gap			SILENT-NONCODING	ATPase_associated	Human Gene SPTREMBL-ID:P97638 SPERMATOGENIC CELL/SPERM-ASSOCIATED TAT-BINDING PROTEIN HOMOLOG SATA - RATTUS NORVEGICUS (RAT), 442 aa.	7.8E-228	11
1034	cg43958825	103	TGAGACTGGGG CTGGCCTGTGTG CC[C/gap]TAGGC GTAGTATTGTAG GTTGGCTT	C	gap			SILENT-NONCODING	ATPase_associated	Human Gene SPTREMBL-ID:P97638 SPERMATOGENIC CELL/SPERM-ASSOCIATED TAT-BINDING PROTEIN HOMOLOG SATA - RATTUS NORVEGICUS (RAT), 442 aa.	7.8E-228	11
1035	cg43958825	38	TTTTTTTTTTTT TTTTTTTTTTT[T/ G]TTTGACCCTA AACCATCTTTTAT T	T	G			SILENT-NONCODING	ATPase_associated	Human Gene SPTREMBL-ID:P97638 SPERMATOGENIC CELL/SPERM-ASSOCIATED TAT-BINDING PROTEIN HOMOLOG SATA - RATTUS NORVEGICUS (RAT), 442 aa.	7.8E-228	11
1036	cg43975309	160	TAGTGTATAGAA CATTTCACAATTA [C/T]ACTCATCTT TTACATAACATCT TGA	C	T			SILENT-NONCODING	ATPase_associated	Human Gene SPTREMBL-ID:Q93529 F18C12.2 - CAENORHABDITIS ELEGANS, 2245 aa.	5.8E-184	3
1037	cg43975309	553	AACAAATGTGCT TACATACACCAA G[A/gap]AAAAA AATTCTTGTGT ACCCACT	A	gap			SILENT-NONCODING	ATPase_associated	Human Gene SPTREMBL-ID:Q93529 F18C12.2 - CAENORHABDITIS ELEGANS, 2245 aa.	5.8E-184	3

1038	cg43300636	224	GGTCAGGAAGG AGGTCTGGCAG GAC[C/gap]TGCA GTGGGCCCTAGT CATCTGTGG	C	gap			SILENT-NONCODING	ATPase_associated	Human Gene SPTREMBL-ID:Q29466 VACUOLAR H+-ATPASE SUBUNIT (EC 3.6.1.34) (H(+)-TRANSPORTING ATP SYNTHASE) (H(+)-TRANSPORTING ATPASE) (MITOCHONDRIAL ATPASE) (COUPLING FACTORS (F(O), F(1) AND CF(1))) - BOS TAURUS (BOVINE), 838 aa.	1.7E-175	
1039	cg43945992	1220	CCGATCTCCACT GTTGGGTGGGT GG[G/gap]CCCTG CCGGGACCCTG CTCACAGGC	G	gap			SILENT-NONCODING	ATPase_associated	Human Gene SWISSPROT-ID:P13686 TARTRATE-RESISTANT ACID PHOSPHATASE TYPE 5 PRECURSOR (EC 3.1.3.2) (TR-AP) (TARTRATE-RESISTANT ACID ATPASE) (TRATPASE) - HOMO SAPIENS (HUMAN), 323 aa.	1.1E-173	19 (19p13.3)
1040	cg43918426	356	GCAGTCGAGCG CCACGGCTGCTC AT[C/T]GGATGAT CCAGGATGGGT CCTTGGC	C	T			SILENT-NONCODING	ATPase_associated	Human Gene SWISSNEW-ID:O42908 HYPOTHETICAL 99.0 KD PROTEIN SPBC119.17 - SCHIZOSACCHAROMYCES POMBE (FISSION YEAST), 882 aa.	4.7E-155	20
1041	cg43918426	427	CGAGGATGGCC AGGCCGTGTGT GCT[C/T]TTCCCA GTGCCGAGGTA CCTATCGC	C	T			SILENT-NONCODING	ATPase_associated	Human Gene SWISSNEW-ID:O42908 HYPOTHETICAL 99.0 KD PROTEIN SPBC119.17 - SCHIZOSACCHAROMYCES POMBE (FISSION YEAST), 882 aa.	4.7E-155	20
1042	cg43918426	445	GTGTGCTCTTCC CAGTGCCGAGG TA[C/T]CTATCGC TCACGGCCAGG AGCTTGT	C	T			SILENT-NONCODING	ATPase_associated	Human Gene SWISSNEW-ID:O42908 HYPOTHETICAL 99.0 KD PROTEIN SPBC119.17 - SCHIZOSACCHAROMYCES POMBE (FISSION YEAST), 882 aa.	4.7E-155	20
1043	cg43991972	193	TTTTTTTTTTTTT TTTTTTTTTTTT[G /T]GCCTTAGAGA GGGCAGTTTTAT TGT	G	T			SILENT-NONCODING	ATPase_associated	Human Gene SPTREMBL-ID:Q25531 40-KDA V-ATPASE SUBUNIT - MANDUCA SEXTA (TOBACCO HAWKMOTH) (TOBACCO HORNWORM), 348 aa.	7.2E-154	

1044	cg43947105	1689	TCTCGTTCTTCG TCATGGTGTGCG C[G/gap]CGGACG GCGAGAGGAGC TGCGGCCG	G	gap			SILENT-NONCODING	ATPase_associated	Human Gene SWISSPROT-ID:P54709 SODIUM/POTASSIUM-TRANSPORTING ATPASE BETA-3 CHAIN (EC 3.6.1.37) (SODIUM/POTASSIUM-DEPENDENT ATPASE) (ATPB-3) - HOMO SAPIENS (HUMAN), 279 aa.	4.6E-152	
1045	cg43947105	1763	GCGGAGGCGCG TCCCGGCTCCG GCG[G/gap]CGCA GCCCGGAGACG GCAGTGAAGG	G	gap			SILENT-NONCODING	ATPase_associated	Human Gene SWISSPROT-ID:P54709 SODIUM/POTASSIUM-TRANSPORTING ATPASE BETA-3 CHAIN (EC 3.6.1.37) (SODIUM/POTASSIUM-DEPENDENT ATPASE) (ATPB-3) - HOMO SAPIENS (HUMAN), 279 aa.	4.60E-152	
1046	cg43947105	492	CTGTTGACATCA AAATATGACAGT T[G/gap]TTATATC CATAAAATATTTA CATAG	G	gap			SILENT-NONCODING	ATPase_associated	Human Gene SWISSPROT-ID:P54709 SODIUM/POTASSIUM-TRANSPORTING ATPASE BETA-3 CHAIN (EC 3.6.1.37) (SODIUM/POTASSIUM-DEPENDENT ATPASE) (ATPB-3) - HOMO SAPIENS (HUMAN), 279 aa.	4.60E-152	
1047	cg43947105	575	TAAACCACATAA AAAGAGGACAAG A[C/A]CCCCATCC TACATGTTTGGA ATCAG	C	A			SILENT-NONCODING	ATPase_associated	Human Gene SWISSPROT-ID:P54709 SODIUM/POTASSIUM-TRANSPORTING ATPASE BETA-3 CHAIN (EC 3.6.1.37) (SODIUM/POTASSIUM-DEPENDENT ATPASE) (ATPB-3) - HOMO SAPIENS (HUMAN), 279 aa.	4.60E-152	
1048	cg43947105	587	AAAGAGGACAAG ACCCCCATCCTA C[A/G]TGTTTGGA ATCAGGTGTTCA CCGGT	A	G			SILENT-NONCODING	ATPase_associated	Human Gene SWISSPROT-ID:P54709 SODIUM/POTASSIUM-TRANSPORTING ATPASE BETA-3 CHAIN (EC 3.6.1.37) (SODIUM/POTASSIUM-DEPENDENT ATPASE) (ATPB-3) - HOMO SAPIENS (HUMAN), 279 aa.	4.60E-152	

1049	cg43947105	609	TACATGTTTGGA ATCAGGTGTTCA C[C/G]GGTCCCT ATCTGGCGACTG TACACT	C	G			SILENT-NONCODING	ATPase_associated	Human Gene SWISSPROT-ID:P54709 SODIUM/POTASSIUM-TRANSPORTING ATPASE BETA-3 CHAIN (EC 3.6.1.37) (SODIUM/POTASSIUM-DEPENDENT ATPASE) (ATPB-3) - HOMO SAPIENS (HUMAN), 279 aa.	4.60E-152	
1050	cg43927442	303	TTGTTTTTTTTTT TTTTTTTTTTTT[T/A]TCCACATTCAG TTCTTTTATTTAA T	T	A			SILENT-NONCODING	ATPase_associated	Human Gene Homologous to SWISSNEW-ID:O15143 ARP2/3 COMPLEX 41 KD SUBUNIT (P41-ARC) - HOMO SAPIENS (HUMAN), 372 aa.\|pcls:SWISSPROT-ID:O15143 ARP2/3 COMPLEX 41 KD SUBUNIT (P41-ARC) - HOMO SAPIENS (HUMAN), 372 aa.	6.40E-146	17
1051	cg43927442	304	TGTTTTTTTTTTT TTTTTTTTTTTT[T/A]CCACATTCAGT TCTTTTATTTAAT T	T	A			SILENT-NONCODING	ATPase_associated	Human Gene Homologous to SWISSNEW-ID:O15143 ARP2/3 COMPLEX 41 KD SUBUNIT (P41-ARC) - HOMO SAPIENS (HUMAN), 372 aa.\|pcls:SWISSPROT-ID:O15143 ARP2/3 COMPLEX 41 KD SUBUNIT (P41-ARC) - HOMO SAPIENS (HUMAN), 372 aa.	6.40E-146	17
1052	cg43972614	146	GTTGTTTTTTTTT TTTTTTTTTTTT[T/A]ATCGAGAATTC ACTGTTTATTTGT G	T	A			SILENT-NONCODING	ATPase_associated	Human Gene Homologous to TREMBLNEW-ID:G2791859 RIBOSOMAL PROTEIN S4 Y ISOFORM - HOMO SAPIENS (HUMAN), 263 aa.	1.00E-140	Y (Yp11.3)
1053	cg43972614	148	TGTTTTTTTTTTT TTTTTTTTTTA[T/A]CGAGAATTCA CTGTTTATTTGT GCA	T	A			SILENT-NONCODING	ATPase_associated	Human Gene Homologous to TREMBLNEW-ID:G2791859 RIBOSOMAL PROTEIN S4 Y ISOFORM - HOMO SAPIENS (HUMAN), 263 aa.	1.00E-140	Y (Yp11.3)
1054	cg43918496	1850	GCTTGCTGGTTT TATTGCAAGAAT A[T/C]AAGTAGCA TTGCAGTAGTCT ACTTT	T	C			SILENT-NONCODING	ATPase_associated	Human Gene Homologous to SWISSPROT-ID:P54813 YME1 PROTEIN HOMOLOG (EC 3.4.24.-) - CAENORHABDITIS ELEGANS, 676 aa.	2.80E-136	10

1055	cg43284434	2578	ATCAGAGAGGAATAAAAAGACATTT[T/gap]ATATTTTATTCTGCTCCATTCCCTT	T	gap			SILENT-NONCODING	ATPase_associated	Human Gene Homologous to SPTREMBL-ID:Q18788 C52E4.5 - CAENORHABDITIS ELEGANS, 590 aa.	4.00E-121	6
1056	cg43284434	2751	GTGGACCTAAATTCCTTATCATATC[C/gap]TTTATTAATTCAGCCAGTGTATCCA	C	gap			SILENT-NONCODING	ATPase_associated	Human Gene Homologous to SPTREMBL-ID:Q18788 C52E4.5 - CAENORHABDITIS ELEGANS, 590 aa.	4.00E-121	6
1057	cg43284434	2877	CTGAATAGAATTGTATAGCGATGAC[C/T]TCTTAATTATAATTTGATTTGACTG	C	T			SILENT-NONCODING	ATPase_associated	Human Gene Homologous to SPTREMBL-ID:Q18788 C52E4.5 - CAENORHABDITIS ELEGANS, 590 aa.	4.00E-121	6
1058	cg43284434	3312	ATACTAGTTAATTTCTTCCATTCCC[C/T]ACTACACAGAGAGGTGAGCTTTCAA	C	T			SILENT-NONCODING	ATPase_associated	Human Gene Homologous to SPTREMBL-ID:Q18788 C52E4.5 - CAENORHABDITIS ELEGANS, 590 aa.	4.00E-121	6
1059	cg43974574	1219	AAACCACTTAAATGTGAAGGAACAA[C/gap]AGCAACAAGACCAGTATGATATACC	C	gap			SILENT-NONCODING	ATPase_associated	Human Gene Homologous to TREMBLNEW-ID:G2687400 VESICLE SOLUBLE NSF ATTACHMENT PROTEIN RECEPTOR - HOMO SAPIENS (HUMAN), 232 aa.	1.40E-116	14
1060	cg43967912	2065	GGAGACTCCGGGAGCCGAAAGTGAA[G/gap]CGGGTCCCGCACCAAGGAGACGTTG	G	gap			SILENT-NONCODING	ATPase_associated	Human Gene Homologous to SPTREMBL-ID:Q22494 SIMILAR TOS. CEREVISIAE VACUOLAR H(+)-ATPASE 54 KD SUBUNIT - CAENORHABDITIS ELEGANS, 470 aa.	5.60E-108	8
1061	cg43954224	3379	GATTTTGTGCATGTAGTTCAGTCTA[C/G]TGTTGGTAGCATGACAGAAAGTGGG	C	G			SILENT-NONCODING	ATPase_associated	Human Gene Homologous to SPTREMBL-ID:Q18788 C52E4.5 - CAENORHABDITIS ELEGANS, 590 aa.	3.70E-103	1

1062	cg43250373	1641	TATGCTGGCTGG AGTGAGGAAAAA A[A/gap]TCGTCC AGGGAGCATTTT CCTCCAT	A	gap			SILENT-NONCODING	ATPase_associated	Human Gene Similar to TREMBLNEW-ID:G2921585 ECTO-ATPASE - MUS MUSCULUS (MOUSE), 495 aa.	1.40E-100	10 (10q24)
1063	cg43250373	2397	CAGTTACAACTC AGGGTCACAAAA A[A/gap]TGCATC TTCCAATGCATA TTTTTAT	A	gap			SILENT-NONCODING	ATPase_associated	Human Gene Similar to TREMBLNEW-ID:G2921585 ECTO-ATPASE - MUS MUSCULUS (MOUSE), 495 aa.	1.40E-100	10 (10q24)
1064	cg43986887	104	AAGTAAAGTGAA TGAACCATTTG T[G/A]ATTAAGAT ACATAGACAGAA CTTCA	G	A			SILENT-NONCODING	ATPase_associated	Human Gene Similar to SPTREMBL-ID:O00393 P97 HOMOLOGOUS PROTEIN - HOMO SAPIENS (HUMAN), 277 aa (fragment).	7.90E-93	16
1065	cg43986887	136	ATACATAGACAG AACTTCAATGTA G[A/gap]AAAAA AAAGACCTTGCT GGGAAAC	A	gap			SILENT-NONCODING	ATPase_associated	Human Gene Similar to SPTREMBL-ID:O00393 P97 HOMOLOGOUS PROTEIN - HOMO SAPIENS (HUMAN), 277 aa (fragment).	7.90E-93	16
1066	cg43986887	145	AGAACTTCAATG TAGAAAAAAAAA A[gap/A]GACCTT GCTGGGAAACA GATGATGA	gap	A			SILENT-NONCODING	ATPase_associated	Human Gene Similar to SPTREMBL-ID:O00393 P97 HOMOLOGOUS PROTEIN - HOMO SAPIENS (HUMAN), 277 aa (fragment).	7.90E-93	16
1067	cg43969125	681	AATGGACAATAA AGGACTGAGGG AG[A/gap]GGGCT AGAAAATGATTG ATTTTTCT	A	gap			SILENT-NONCODING	ATPase_associated	Human Gene Similar to SWISSPROT-ID:P18708 VESICULAR-FUSION PROTEIN NSF (N-ETHYLMALEIMIDE-SENSITIVE FUSION PROTEIN) (NEM-SENSITIVE FUSION PROTEIN) - CRICETULUS GRISEUS (CHINESE HAMSTER), 744 aa.	1.40E-79	17
1068	cg43972161	186	TTTTTTTTTTTTT TTTTTTTTTTTT[T/A]AAAATTTTAAA TCTTTAATTTCCG T	T	A			SILENT-NONCODING	ATPase_associated	Human Gene Similar to SPTREMBL-ID:Q21221 K04G2.2 - CAENORHABDITIS ELEGANS, 405 aa.	4.70E-79	

1069	cg43972161	306	AGCCCCTGGGT CGGGGCGGGGT CCC[C/gap]TGGG CCGCCCGGGGG GTCCACATGC	C	gap			SILENT-NONCODING	ATPase_associated	Human Gene Similar to SPTREMBL-ID:Q21221 K04G2.2 - CAENORHABDITIS ELEGANS, 405 aa.	4.70E-79	
1070	cg43972161	314	GGTCGGGGCGG GGTCCCCTGGG CCG[C/gap]CCGG GGGGTCCACAT GCAGCCCCTG	C	gap			SILENT-NONCODING	ATPase_associated	Human Gene Similar to SPTREMBL-ID:Q21221 K04G2.2 - CAENORHABDITIS ELEGANS, 405 aa.	4.70E-79	
1071	cg43972161	316	TCGGGGCGGGG TCCCCTGGGCC GCC[C/gap]GGGG GGTCCACATGCA GCCCCTGGG	C	gap			SILENT-NONCODING	ATPase_associated	Human Gene Similar to SPTREMBL-ID:Q21221 K04G2.2 - CAENORHABDITIS ELEGANS, 405 aa.	4.70E-79	
1072	cg43972161	342	GGGGGGTCCAC ATGCAGCCCCTG GG[T/gap]GGGGG CCGGCGCGGGG TGAGGTCCG	T	gap			SILENT-NONCODING	ATPase_associated	Human Gene Similar to SPTREMBL-ID:Q21221 K04G2.2 - CAENORHABDITIS ELEGANS, 405 aa.	4.70E-79	
1073	cg43972161	405	TTGCTGAGGTCC GGCCGGTTGGG GC[C/gap]GCCGC TAGGCGCGCTG GCTGGGCAG	C	gap			SILENT-NONCODING	ATPase_associated	Human Gene Similar to SPTREMBL-ID:Q21221 K04G2.2 - CAENORHABDITIS ELEGANS, 405 aa.	4.70E-79	
1074	cg43943233	1023	GCAAGCAAAAAC AAAGCTATAACT T[G/A]GCAGTGG TATTCACCCACC ACTTAT	G	A			SILENT-NONCODING	ATPase_associated	Human Gene Similar to SWISSPROT-ID:O15511 ARP2/3 COMPLEX 16 KD SUBUNIT (P16-ARC) - HOMO SAPIENS (HUMAN), 151 aa.	3.90E-75	

1075	cg43943233	320	TATCAAAAACAG CAAAGAGTTTAT A[A/G]AATTTCTG CACCAGTTTGCA CATAA	A	G			SILENT-NONCODING	ATPase_associated	Human Gene Similar to SWISSPROT-ID:O15511 ARP2/3 COMPLEX 16 KD SUBUNIT (P16-ARC) - HOMO SAPIENS (HUMAN), 151 aa.	3.90E-75	
1076	cg43917062	179	GGAGACAAATAC ACAAATAACTAG A[A/T]TACAAGGC AGTAAACAAGAG TGGGC	A	T			SILENT-NONCODING	ATPase_associated	Human Gene Similar to SWISSNEW-ID:O42945 PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE SPBC16H5.10C - SCHIZOSACCHAROMYCES POMBE (FISSION YEAST), 735 aa.	6.10E-65	17
1077	cg43917062	76	ACTGAGTGACTA CTATGTGCAAAG C[A/gap]CTATGC TAGGTGCATGAA AGATACA	A	gap			SILENT-NONCODING	ATPase_associated	Human Gene Similar to SWISSNEW-ID:O42945 PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE SPBC16H5.10C - SCHIZOSACCHAROMYCES POMBE (FISSION YEAST), 735 aa.	6.10E-65	17
1078	cg44022155	1279	GAGAGCTGGCC GAGCAGCCCTG GCC[A/G]CCGCT GCCCGCCGGCC CCCTGAGGT	A	G			SILENT-NONCODING	ATPase_associated	Human Gene Similar to SWISSPROT-ID:Q12697 PROBABLE CALCIUM-TRANSPORTING ATPASE 9 (EC 3.6.1.38) - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 1472 aa.	1.50E-63	1
1079	cg44015998	172	AGCCAGCGGAT GGCTGTGGGGG TCC[C/gap]AGCT CAGTCTTCCAAG GGCGAGACT	C	gap			SILENT-NONCODING	ATPase_associated	Human Gene Similar to SWISSPROT-ID:P39986 PROBABLE CALCIUM-TRANSPORTING ATPASE 6 (EC 3.6.1.38) - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 1215 aa.	1.50E-53	
1080	cg44015998	268	GCCCTGTTGGG GTTCCCGCCCAG CG[G/gap]CAGCC AGGGTGGGCAG TGGGTACCA	G	gap			SILENT-NONCODING	ATPase_associated	Human Gene Similar to SWISSPROT-ID:P39986 PROBABLE CALCIUM-TRANSPORTING ATPASE 6 (EC 3.6.1.38) - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 1215 aa.	1.50E-53	

1081	cg43917679	327	CAAGAAGGGAAAAGGATTTATTAGA[C/T]CATTTCCAGGACAGGGACCCAGGGG	C	T			SILENT-NONCODING	ATPase_associated	Human Gene Similar to SWISSPROT-ID:P46467 SKD1 PROTEIN - MUS MUSCULUS (MOUSE), 444 aa.	4.30E-53	16
1082	cg43917679	549	CAGAGCTTGGGCTGGGGTTGCAGGG[G/gap]CATCAGCCAATCTGCTCTCAAGGAG	G	gap			SILENT-NONCODING	ATPase_associated	Human Gene Similar to SWISSPROT-ID:P46467 SKD1 PROTEIN - MUS MUSCULUS (MOUSE), 444 aa.	4.30E-53	16
1083	cg43917679	837	GTAGGAAGAGCAGTGTCCACTGTGT[G/gap]CCCCAGGGCAGTGGAGTGTCTCTGT	G	gap			SILENT-NONCODING	ATPase_associated	Human Gene Similar to SWISSPROT-ID:P46467 SKD1 PROTEIN - MUS MUSCULUS (MOUSE), 444 aa.	4.30E-53	16
1084	cg43966234	2339	AAAAATCACCAATGGAAATTTTCAT[T/gap]GATATAAATACTTGTACATATGATT	T	gap			SILENT-NONCODING	biotindep	Human Gene SWISSPROT-ID:P05165 PROPIONYL-COA CARBOXYLASE ALPHA CHAIN PRECURSOR (EC 6.4.1.3) (PCCASE) (PROPANOYL-COA:CARBON DIOXIDE LIGASE) - HOMO SAPIENS (HUMAN), 702 aa.	0.00E+00	13 (13q32)
1085	cg43966234	2357	TTTTCATTGATATAAATACTTGTAC[A/gap]TATGATTTGTACTTCTGCTGTGAGA	A	gap			SILENT-NONCODING	biotindep	Human Gene SWISSPROT-ID:P05165 PROPIONYL-COA CARBOXYLASE ALPHA CHAIN PRECURSOR (EC 6.4.1.3) (PCCASE) (PROPANOYL-COA:CARBON DIOXIDE LIGASE) - HOMO SAPIENS (HUMAN), 702 aa.	0.00E+00	13 (13q32)
1086	cg43966234	2363	TTGATATAAATACTTGTACATATGA[T/G]TTGTACTTCTGCTGTGAGATTCCCT	T	G			SILENT-NONCODING	biotindep	Human Gene SWISSPROT-ID:P05165 PROPIONYL-COA CARBOXYLASE ALPHA CHAIN PRECURSOR (EC 6.4.1.3) (PCCASE) (PROPANOYL-COA:CARBON DIOXIDE LIGASE) - HOMO SAPIENS (HUMAN), 702 aa.	0.00E+00	13 (13q32)

1087	cg43009431	3003	CTCCCCAAACGGCGGTAATGCCGGG[C/gap]GTCCCCGAGACGCGGCTGCCTGTCC	C	gap			SILENT-NONCODING	biotindep	Human Gene SWISSPROT-ID:P50747 BIOTIN--PROTEIN LIGASE (EC 6.3.4.-) (BIOTIN APO-PROTEIN LIGASE) (BIOTIN--[METHYLMALONYL-COA-CARBOXYLTRANSFERASE] LIGASE (EC 6.3.4.9) / BIOTIN--[PROPIONYL-COA-CARBOXYLASE (ATP-HYDROLYSING)] LIGASE (EC 6.3.4.10) (HOLOCARBOXYLASE SYNTHETASE) (HCS) / BIOTIN-- [METHYLCROTONOYL COA-CARBOXYLASE] LIGASE (EC 6.3.4.11) / BIOTIN-- [ACETYL-COA-CARBOXYLASE] LIGASE (EC 6.3.4.15)) HOMO SAPIENS (HUMAN), 726 aa.	0.00E+00	21 (21q22.1)
1088	cg43920913	1770	CCATTCCTGCCTTTTGCAATCATGA[A/T]ACCTGGGAATCCAAATAGTTGGATA	A	T			SILENT-NONCODING	biotindep	Human Gene SWISSPROT-ID:P05166 PROPIONYL-COA CARBOXYLASE BETA CHAIN PRECURSOR (EC 6.4.1.3) (PCCASE) (PROPANOYL-COA:CARBON DIOXIDE LIGASE) - HOMO SAPIENS (HUMAN), 539 aa.	8.20E-288	3 (3q21)
1089	cg43920913	1777	TGCCTTTTGCAATCATGAAACCTGG[G/C]AATCCAAATAGTTGGATAACTTAGA	G	C			SILENT-NONCODING	biotindep	Human Gene SWISSPROT-ID:P05166 PROPIONYL-COA CARBOXYLASE BETA CHAIN PRECURSOR (EC 6.4.1.3) (PCCASE) (PROPANOYL-COA:CARBON DIOXIDE LIGASE) - HOMO SAPIENS (HUMAN), 539 aa.	8.20E-288	3 (3q21)
1090	cg43920913	1788	TCATGAAACCTGGGAATCCAAATAG[gap/G]TTGGATAACTTAGAATAACTAAGTT	gap	G			SILENT-NONCODING	biotindep	Human Gene SWISSPROT-ID:P05166 PROPIONYL-COA CARBOXYLASE BETA CHAIN PRECURSOR (EC 6.4.1.3) (PCCASE) (PROPANOYL-COA:CARBON DIOXIDE LIGASE) - HOMO SAPIENS (HUMAN), 539 aa.	8.20E-288	3 (3q21)

1091	cg43920913	1796	CCTGGGAATCCAAATAGTTGGATAA[gap/G]CTTAGAATAACTAAGTTTATTTAAAT	gap	G			SILENT-NONCODING	biotindep	Human Gene SWISSPROT-ID:P05166 PROPIONYL-COA CARBOXYLASE BETA CHAIN PRECURSOR (EC 6.4.1.3) (PCCASE) (PROPANOYL-COA:CARBON DIOXIDE LIGASE) - HOMO SAPIENS (HUMAN), 539 aa.	8.20E-288	3 (3q21)
1092	cg43920913	1801	GGAATCCAAATAGTTGGATAACTTA[G/T]AATAACTAAGTTTATTAAATTCTAG	G	T			SILENT-NONCODING	biotindep	Human Gene SWISSPROT-ID:P05166 PROPIONYL-COA CARBOXYLASE BETA CHAIN PRECURSOR (EC 6.4.1.3) (PCCASE) (PROPANOYL-COA:CARBON DIOXIDE LIGASE) - HOMO SAPIENS (HUMAN), 539 aa.	8.20E-288	3 (3q21)
1093	cg43920913	1809	AATAGTTGGATAACTTAGAATAACT[A/G]AGTTTATTAAATTCTAGAAAGATAA	A	G			SILENT-NONCODING	biotindep	Human Gene SWISSPROT-ID:P05166 PROPIONYL-COA CARBOXYLASE BETA CHAIN PRECURSOR (EC 6.4.1.3) (PCCASE) (PROPANOYL-COA:CARBON DIOXIDE LIGASE) - HOMO SAPIENS (HUMAN), 539 aa.	8.2E-288	3 (3q21)
1094	cg43931765	665	GCCAGGTGACATGGCCAGGCACCTT[gap/C]CCTGTACAGGCACTGTGGGCTCCTG	gap	C			SILENT-NONCODING	cadherin	Human Gene SWISSPROT-ID:P18084 INTEGRIN BETA-5 SUBUNIT PRECURSOR - HOMO SAPIENS (HUMAN), 799 aa.	0	3
1095	cg43931765	692	CTGTACAGGCACTGTGGGCTCCTGG[C/gap]CCAGGCTCACTAGAAGGTCTTCTCT	C	gap			SILENT-NONCODING	cadherin	Human Gene SWISSPROT-ID:P18084 INTEGRIN BETA-5 SUBUNIT PRECURSOR - HOMO SAPIENS (HUMAN), 799 aa.	0	3
1096	cg43918042	1005	TTAGAAGGAGCAGTAGCAGCAGCAG[C/gap]AGGAGAAGATGCTGAGGATGCGGAC	C	gap			SILENT-NONCODING	cadherin	Human Gene TREMBLNEW-ID:G2852363 NF-PROTOCADHERIN - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 1035 aa.	0	4
1097	cg43265972	2272	TGATGAGTTCATTAGCTAAGTTAAA[A/gap]TTAATTTGAACTTTGATCTAAACCA	A	gap			SILENT-NONCODING	cadherin	Human Gene SPTREMBL-ID:Q08192 PROTOCADHERIN 43 (PC43) (CADHERIN-LIKE PROTEIN) - HOMO SAPIENS (HUMAN), 904 aa.	0.00E+00	5

1098	cg43265972	2279	TTCATTAGCTAA GTTAAAATTAATT [T/gap]GAACTTT GATCTAAACCAA AACAAA	T	gap			SILENT-NONCODING	cadherin	Human Gene SPTREMBL-ID:Q08192 PROTOCADHERIN 43 (PC43) (CADHERIN-LIKE PROTEIN) - HOMO SAPIENS (HUMAN), 904 aa.	0.00E+00	5
1099	cg43265972	2333	GGAAAATAAAGC TGTAAAGGAACT T[T/gap]ATCAAG CATTCCAAAACC AACTAGA	T	gap			SILENT-NONCODING	cadherin	Human Gene SPTREMBL-ID:Q08192 PROTOCADHERIN 43 (PC43) (CADHERIN-LIKE PROTEIN) - HOMO SAPIENS (HUMAN), 904 aa.	0.00E+00	5
1100	cg43265972	2374	ACCAACTAGAAA TTACTTGAAGTTT [T/gap]CGAGTGA GCATTGCCTGTG CCAGTA	T	gap			SILENT-NONCODING	cadherin	Human Gene SPTREMBL-ID:Q08192 PROTOCADHERIN 43 (PC43) (CADHERIN-LIKE PROTEIN) - HOMO SAPIENS (HUMAN), 904 aa.	0.00E+00	5
1101	cg43265972	2494	TATTCAGCCAAT TTCATGGATGTA A[A/gap]CGATGG ATATAAATAATTG ATAGCA	A	gap			SILENT-NONCODING	cadherin	Human Gene SPTREMBL-ID:Q08192 PROTOCADHERIN 43 (PC43) (CADHERIN-LIKE PROTEIN) - HOMO SAPIENS (HUMAN), 904 aa.	0.00E+00	5
1102	cg43968898	212	ACGGGGGAGGG GGTCGCCTTAGC GC[G/gap]TGGAC ACAGCACAAAAC ACAACACG	G	gap			SILENT-NONCODING	cadherin	Human Gene SPTREMBL-ID:Q08192 PROTOCADHERIN 43 (PC43) (CADHERIN-LIKE PROTEIN) - HOMO SAPIENS (HUMAN), 904 aa.	0.00E+00	5
1103	cg43976826	1294	ACTGTCTTATTTT TATTTTCATGTT[gap/T]CCTTCTTT TCCCAGCATTGC AGTTT	gap	T			SILENT-NONCODING	cadherin	Human Gene TREMBLNEW-ID:G1881841 R NR-CAM 22=NEUROFASCIN HOMOLOG/IG-FNIII CELL ADHESION MOLECULE {ALTERNATIVELY SPLICED} - RATTUS SP, 1166 aa.	0.00E+00	7
1104	cg43976826	1638	TGTAATGCCTGG AAGATTAAGAAG C[C/gap]TACGGA GTAACAGGAGCC AAGAGTA	C	gap			SILENT-NONCODING	cadherin	Human Gene TREMBLNEW-ID:G1881841 R NR-CAM 22=NEUROFASCIN HOMOLOG/IG-FNIII CELL ADHESION MOLECULE {ALTERNATIVELY SPLICED} - RATTUS SP, 1166 aa.	0.00E+00	7

1105	cg43952088	4171	ACAACCCACCAAAGTTTCCGCAGAG[C/G]GTATACCAGATGTCTGTGTCAGAAG	C	G			SILENT-NONCODING	cadherin	Human Gene SPTREMBL-ID:Q15065 OB CADHERIN-1 - HOMO SAPIENS (HUMAN), 796 aa.	0.00E+00	16
1106	cg43952088	4172	CAACCCACCAAAGTTTCCGCAGAGC[G/C]TATACCAGATGTCTGTGTCAGAAGC	G	C			SILENT-NONCODING	cadherin	Human Gene SPTREMBL-ID:Q15065 OB CADHERIN-1 - HOMO SAPIENS (HUMAN), 796 aa.	0.00E+00	16
1107	cg43952088	4376	GAAAAAGCCTGTAGATTTTGAAACC[A/G]AAAGAGCCTATAGCTTGAAGGTAGA	A	G			SILENT-NONCODING	cadherin	Human Gene SPTREMBL-ID:Q15065 OB CADHERIN-1 - HOMO SAPIENS (HUMAN), 796 aa.	0.00E+00	16
1108	cg43952088	4475	CAAGGACACTGTGACCGTCAAGATC[G/T]CAGTAGAAGATGCTGATGAGCCCCC	G	T			SILENT-NONCODING	cadherin	Human Gene SPTREMBL-ID:Q15065 OB CADHERIN-1 - HOMO SAPIENS (HUMAN), 796 aa.	0.00E+00	16
1109	cg43127783	4451	GGCTTCAGGGCGCACAGCATGAGAG[G/C]CTCTGTGCCCCCATCACCCTCGTTT	G	C			SILENT-NONCODING	cadherin	Human Gene SWISSPROT-ID:P20702 LEUKOCYTE ADHESION GLYCOPROTEIN P150,95 ALPHA CHAIN PRECURSOR (LEUKOCYTE ADHESION RECEPTOR P150,95) (CD11C) (LEU M5) (INTEGRIN ALPHA-X) - HOMO SAPIENS (HUMAN), 1163 aa.	0.00E+00	16 (16p11.2)
1110	cg43127783	4541	CATCGTGGGGCTCTCAGTTCCGATT[T/C]CCCAGGCTGAATTGGGAGTGAGATG	T	C			SILENT-NONCODING	cadherin	Human Gene SWISSPROT-ID:P20702 LEUKOCYTE ADHESION GLYCOPROTEIN P150,95 ALPHA CHAIN PRECURSOR (LEUKOCYTE ADHESION RECEPTOR P150,95) (CD11C) (LEU M5) (INTEGRIN ALPHA-X) - HOMO SAPIENS (HUMAN), 1163 aa.	0.00E+00	16 (16p11.2)

1111	cg43127783	4602	GGTTCTGCACAGCTGGCCTCCCGCG[gap/G]TTGGGCAACATTGCTGGCTGGAAGG	gap	G			SILENT-NONCODING	cadherin	Human Gene SWISSPROT-ID:P20702 LEUKOCYTE ADHESION GLYCOPROTEIN P150,95 ALPHA CHAIN PRECURSOR (LEUKOCYTE ADHESION RECEPTOR P150,95) (CD11C) (LEU M5) (INTEGRIN ALPHA-X) - HOMO SAPIENS (HUMAN), 1163 aa.	0.00E+00	16 (16p11.2)
1112	cg43127783	4607	TGCACAGCTGGCCTCCCGCGTTGGG[gap/T]CAACATTGCTGGCTGGAAGGGAGGA	gap	T			SILENT-NONCODING	cadherin	Human Gene SWISSPROT-ID:P20702 LEUKOCYTE ADHESION GLYCOPROTEIN P150,95 ALPHA CHAIN PRECURSOR (LEUKOCYTE ADHESION RECEPTOR P150,95) (CD11C) (LEU M5) (INTEGRIN ALPHA-X) - HOMO SAPIENS (HUMAN), 1163 aa.	0.00E+00	16 (16p11.2)
1113	cg43127783	4620	TCCCGCGTTGGGCAACATTGCTGGC[gap/C]TGGAAGGGAGGAGCGCCCTCTAGGG	gap	C			SILENT-NONCODING	cadherin	Human Gene SWISSPROT-ID:P20702 LEUKOCYTE ADHESION GLYCOPROTEIN P150,95 ALPHA CHAIN PRECURSOR (LEUKOCYTE ADHESION RECEPTOR P150,95) (CD11C) (LEU M5) (INTEGRIN ALPHA-X) - HOMO SAPIENS (HUMAN), 1163 aa.	0.00E+00	16 (16p11.2)
1114	cg43127783	4679	GGCCCCGGTGCGGCTGCAGCTCACC[C/gap]AGCCCCAGGGGCAGAAGAGACCCAA	C	gap			SILENT-NONCODING	cadherin	Human Gene SWISSPROT-ID:P20702 LEUKOCYTE ADHESION GLYCOPROTEIN P150,95 ALPHA CHAIN PRECURSOR (LEUKOCYTE ADHESION RECEPTOR P150,95) (CD11C) (LEU M5) (INTEGRIN ALPHA-X) - HOMO SAPIENS (HUMAN), 1163 aa.	0.00E+00	16 (16p11.2)

1115	cg43127783	4756	ATATAGTACCTGAAAAAATGCCAAG[C/gap]ACAAGATTATTTTTTTAAAAAGCGT	C	gap			SILENT-NONCODING	cadherin	Human Gene SWISSPROT-ID:P20702 LEUKOCYTE ADHESION GLYCOPROTEIN P150,95 ALPHA CHAIN PRECURSOR (LEUKOCYTE ADHESION RECEPTOR P150,95) (CD11C) (LEU M5) (INTEGRIN ALPHA-X) - HOMO SAPIENS (HUMAN), 1163 aa.	0.00E+00	16 (16p11.2)
1116	cg43127783	4759	TAGTACCTGAAAAAATGCCAAGCAC[A/T]AGATTATTTTTTTAAAAAGCGTACT	A	T			SILENT-NONCODING	cadherin	Human Gene SWISSPROT-ID:P20702 LEUKOCYTE ADHESION GLYCOPROTEIN P150,95 ALPHA CHAIN PRECURSOR (LEUKOCYTE ADHESION RECEPTOR P150,95) (CD11C) (LEU M5) (INTEGRIN ALPHA-X) - HOMO SAPIENS (HUMAN), 1163 aa.	0.00E+00	16 (16p11.2)
1117	cg43127783	4760	AGTACCTGAAAAAATGCCAAGCACA[A/T]GATTATTTTTTTAAAAAGCGTACTT	A	T			SILENT-NONCODING	cadherin	Human Gene SWISSPROT-ID:P20702 LEUKOCYTE ADHESION GLYCOPROTEIN P150,95 ALPHA CHAIN PRECURSOR (LEUKOCYTE ADHESION RECEPTOR P150,95) (CD11C) (LEU M5) (INTEGRIN ALPHA-X) - HOMO SAPIENS (HUMAN), 1163 aa.	0.00E+00	16 (16p11.2)
1118	cg44026923	187	GCTCTGTGCATGCGGGTGGGCTGGG[gap/C]CCCCAGGGGTGCAAGGATGGAGTAG	gap	C			SILENT-NONCODING	cadherin	Human Gene SWISSPROT-ID:P16144 INTEGRIN BETA-4 SUBUNIT PRECURSOR (GP150) (CD104) - HOMO SAPIENS (HUMAN), 1875 aa.	0.00E+00	17 (17q11)
1119	cg44026923	191	CTGTGCATGCGGGTGGGCTGGGCCC[C/gap]AGGGGTGCAAGGATGGAGTAGCTGA	C	gap			SILENT-NONCODING	cadherin	Human Gene SWISSPROT-ID:P16144 INTEGRIN BETA-4 SUBUNIT PRECURSOR (GP150) (CD104) - HOMO SAPIENS (HUMAN), 1875 aa.	0	17 (17q11)

1120	cg44026923	258	GAGTCGGGAGG ACGCCTAGTGG GAC[A/G]TGGCG GGGGTGGGGCA GGGTGCGGT	A	G		SILENT-NONCODING	cadherin	Human Gene SWISSPROT-ID:P16144 INTEGRIN BETA-4 SUBUNIT PRECURSOR (GP150) (CD104) - HOMO SAPIENS (HUMAN), 1875 aa.	0	17 (17q11)
1121	cg42558238	2838	CACGCCACATG GCTTCCTCCTGC G[C/T]GCATGTG CGCACACACACA CACACA	C	T		SILENT-NONCODING	cadherin	Human Gene SWISSNEW-ID:Q01665 B-CELL RECEPTOR CD22-BETA PRECURSOR (LEU-14) (B-LYMPHOCYTE CELL ADHESION MOLECULE) (BL-CAM) - HOMO SAPIENS (HUMAN), 847 aa.\|pcls:SWISSPROT-ID:Q01665 B-CELL RECEPTOR CD22-BETA PRECURSOR (LEU-14) (B-LYMPHOCYTE CELL ADHESION MOLECULE) (BL-CAM) - HOMO SAPIENS (HUMAN), 847 aa.	0	19 (19q13.1)
1122	cg42558238	2999	CCACTCTCCTTG CTACCCAGAAAT C[C/gap]ATCTAA ATACCTGCCCTG ACATGCA	C	gap		SILENT-NONCODING	cadherin	Human Gene SWISSNEW-ID:Q01665 B-CELL RECEPTOR CD22-BETA PRECURSOR (LEU-14) (B-LYMPHOCYTE CELL ADHESION MOLECULE) (BL-CAM) - HOMO SAPIENS (HUMAN), 847 aa.\|pcls:SWISSPROT-ID:Q01665 B-CELL RECEPTOR CD22-BETA PRECURSOR (LEU-14) (B-LYMPHOCYTE CELL ADHESION MOLECULE) (BL-CAM) - HOMO SAPIENS (HUMAN), 847 aa.	0	19 (19q13.1)

1123	cg42558238	3220	GGGAAAGCCCA GAAAAGGACAGA AA[C/T]GAAGTAG AAAGGGGCCCA GTCCTGG	C	T		SILENT-NONCODING	cadherin	Human Gene SWISSNEW-ID:Q01665 B-CELL RECEPTOR CD22-BETA PRECURSOR (LEU-14) (B-LYMPHOCYTE CELL ADHESION MOLECULE) (BL-CAM) - HOMO SAPIENS (HUMAN), 847 aa.	pcls:SWISSPROT-ID:Q01665 B-CELL RECEPTOR CD22-BETA PRECURSOR (LEU-14) (B-LYMPHOCYTE CELL ADHESION MOLECULE) (BL-CAM) - HOMO SAPIENS (HUMAN), 847 aa.	0	19 (19q13.1)
1124	cg43994411	1460	TCTTCAGAAAGT AGGCTTTCAAAT T[A/G]CTCTTCTC CATATTTTTGTAG ATAT	A	G		SILENT-NONCODING	cadherin	Human Gene SWISSNEW-ID:P06756 VITRONECTIN RECEPTOR ALPHA SUBUNIT PRECURSOR (INTEGRIN ALPHA-V) (CD51) - HOMO SAPIENS (HUMAN), 1048 aa.	pcls:SWISSPROT-ID:P06756 VITRONECTIN RECEPTOR ALPHA SUBUNIT PRECURSOR (INTEGRIN ALPHA-V) (CD51) - HOMO SAPIENS (HUMAN), 1048 aa.	0	2 (2q31)
1125	cg43994411	1714	CAACATATTTTCA GAAATGACTGTT[A/G]CTAGGTGGT AAAACTGTTAGG GTAA	A	G		SILENT-NONCODING	cadherin	Human Gene SWISSNEW-ID:P06756 VITRONECTIN RECEPTOR ALPHA SUBUNIT PRECURSOR (INTEGRIN ALPHA-V) (CD51) - HOMO SAPIENS (HUMAN), 1048 aa.	pcls:SWISSPROT-ID:P06756 VITRONECTIN RECEPTOR ALPHA SUBUNIT PRECURSOR (INTEGRIN ALPHA-V) (CD51) - HOMO SAPIENS (HUMAN), 1048 aa.	0	2 (2q31)
1126	cg43994411	393	ATACAAATATTTG TTTATATTAGGC[T/C]TACTAAATTA ATGACAACTTTG AAA	T	C		SILENT-NONCODING	cadherin	Human Gene SWISSNEW-ID:P06756 VITRONECTIN RECEPTOR ALPHA SUBUNIT PRECURSOR (INTEGRIN ALPHA-V) (CD51) - HOMO SAPIENS (HUMAN), 1048 aa.	pcls:SWISSPROT-ID:P06756 VITRONECTIN RECEPTOR ALPHA SUBUNIT PRECURSOR (INTEGRIN ALPHA-V) (CD51) - HOMO SAPIENS (HUMAN), 1048 aa.	0	2 (2q31)

1127	cg43980086	250	CCAAGTCCCAGGACTGGCTGATAGC[C/gap]TCTCCCAGTGGATAGCAGGTCCTAA	C	gap			SILENT-NONCODING	cadherin	Human Gene SWISSNEW-ID:P38570 INTEGRIN ALPHA-E PRECURSOR (MUCOSAL LYMPHOCYTE-1 ANTIGEN) (HML-1 ANTIGEN) (CD103 ANTIGEN) (INTEGRIN ALPHA-IEL) - HOMO SAPIENS (HUMAN), 1178 aa.\|pcls:SWISSPROT-ID:P38570 INTEGRIN ALPHA-E PRECURSOR (MUCOSAL LYMPHOCYTE-1 ANTIGEN) (HML-1 ANTIGEN) (CD103 ANTIGEN) (INTEGRIN ALPHA-IEL) - HOMO SAPIENS (HUMAN), 1178 aa.	0	
1128	cg43948700	159	AAGCTCTGAGCCCGCCCCTCTTGGG[C/gap]CACAGTGGTAGGGATGGGGGAAGGG	C	gap			SILENT-NONCODING	cadherin	Human Gene TREMBLNEW-ID:G2739450 INTEGRIN BINDING PROTEIN KINASE - MUS MUSCULUS (MOUSE), 452 aa.	4.9E-251	11
1129	cg43948700	204	GAAGGGGATGGACCCCATGGCTGGG[G/gap]TAGTACCATGACTGGAGGCGGGGGGA	G	gap			SILENT-NONCODING	cadherin	Human Gene TREMBLNEW-ID:G2739450 INTEGRIN BINDING PROTEIN KINASE - MUS MUSCULUS (MOUSE), 452 aa.	4.90E-251	11
1130	cg43949264	14175	ATCGTGAGGTTTTCATCGGCTGTGC[gap/C]ATTTCCCAACGTCTTTTGGGATTTA	gap	C			SILENT-NONCODING	cadherin	Human Gene SWISSPROT-ID:P33450 CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN) - DROSOPHILA MELANOGASTER (FRUIT FLY), 5147 aa.	6.20E-222	4
1131	cg43949264	14400	TTGTTTCAACTGAATTTTGGTGGTG[G/T]TAGTGCCATTATCTAGCACCCTGAT	G	T			SILENT-NONCODING	cadherin	Human Gene SWISSPROT-ID:P33450 CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN) - DROSOPHILA MELANOGASTER (FRUIT FLY), 5147 aa.	6.20E-222	4

1132	cg43949264	14436	ATCTAGCACCCT GATTTTTTTTTTT[T/gap]ACTATAAC CAGGGTTTCATT CTGTC	T	gap			SILENT-NONCODING	cadherin	Human Gene SWISSPROT-ID:P33450 CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN) - DROSOPHILA MELANOGASTER (FRUIT FLY), 5147 aa.	6.20E-222	4
1133	cg43949264	14436	TCTAGCACCCTG ATTTTTTTTTTT[gap/T]ACTATAAC CAGGGTTTCATT CTGTC	gap	T			SILENT-NONCODING	cadherin	Human Gene SWISSPROT-ID:P33450 CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN) - DROSOPHILA MELANOGASTER (FRUIT FLY), 5147 aa.	6.20E-222	4
1134	cg43956560	1579	TTCTGAGGAGAA ACAAATAAGACC A[T/C]AAAGGGAA AGGATTCATGTG GAATA	T	C			SILENT-NONCODING	cadherin	Human Gene SWISSPROT-ID:P14151 L-SELECTIN PRECURSOR (LYMPH NODE HOMING RECEPTOR) (LEUKOCYTE ADHESION MOLECULE-1) (LAM-1) (LEUKOCYTE SURFACE ANTIGEN LEU-8) (TQ1) (GP90-MEL) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 1) (LECAM1) (CD62L) - HOMO SAPIENS (HUMAN), 372 aa.	1.00E-218	1 (1q23)
1135	cg42701303	989	GTGGCTCCACTT GCCCGTCTGCTT G[G/gap]CCCCAG GCTGCTCTTGTC CTGTTTG	G	gap			SILENT-NONCODING	cadherin	Human Gene SWISSPROT-ID:Q14242 P SELECTIN GLYCOPROTEIN LIGAND 1 PRECURSOR (PSGL-1) (SELECTIN P LIGAND) (CD162 ANTIGEN) - HOMO SAPIENS (HUMAN), 412 aa.	2.50E-215	12 (12q24)
1136	cg42701303	1083	CTCCGAGGAAG CCCAGAGCTGTG GA[A/T]TGGGGT CTGGGCACTCAG GGGTGGC	A	T			SILENT-NONCODING	cadherin	Human Gene SWISSPROT-ID:Q14242 P SELECTIN GLYCOPROTEIN LIGAND 1 PRECURSOR (PSGL-1) (SELECTIN P LIGAND) (CD162 ANTIGEN) - HOMO SAPIENS (HUMAN), 412 aa.	2.50E-215	12 (12q24)

1137	cg43977724	1602	TCATTCCCAACA ACATCCTCTGCC A[C/T]ACACAACA AAACGTAAGTTT CATTT	C	T			SILENT-NONCODING	cadherin	Human Gene SWISSPROT-ID:Q14982 OPIOID BINDING PROTEIN/CELL ADHESION MOLECULE PRECURSOR (OBCAM) (OPIOID-BINDING CELL ADHESION MOLECULE) (OPCML) - HOMO SAPIENS (HUMAN), 345 aa.	1.80E-182	11
1138	cg43956666	1161	AGTAAGACGTGA AAGGAATACACT T[G/C]TGTTTAAG CACCATGGCCTT GATGA	G	C			SILENT-NONCODING	cadherin	Human Gene SWISSNEW-ID:Q08722 LEUKOCYTE SURFACE ANTIGEN CD47 PRECURSOR (ANTIGENIC SURFACE DETERMINANT PROTEIN OA3) (INTEGRIN ASSOCIATED PROTEIN) (IAP) (MER6) - HOMO SAPIENS (HUMAN), 323 aa.\|pcls:SWISSPROT-ID:Q08722 LEUKOCYTE SURFACE ANTIGEN CD47 PRECURSOR (ANTIGENIC SURFACE DETERMINANT PROTEIN OA3) (INTEGRIN ASSOCIATED PROTEIN) (IAP) (MER6) - HOMO SAPIENS (HUMAN), 323 aa.	1.20E-167	3 (3q13.1)
1139	cg43943478	366	GAGGAGAGGCC CTGACAACGAGG GC[C/gap]GCCCC TGCCCGGGGTG AGGCTGCAC	C	gap			SILENT-NONCODING	cadherin	Human Gene Similar to SPTREMBL-ID:Q99971 CALCIUM AND INTEGRIN BINDING PROTEIN CIB - HOMO SAPIENS (HUMAN), 191 aa.	1.50E-96	
1140	cg43943478	398	CCCGGGGTGAG GCTGCACAGCG CCA[gap/G]CTCC AGGCTGGGCCA GCTTGGCCCG	gap	G			SILENT-NONCODING	cadherin	Human Gene Similar to SPTREMBL-ID:Q99971 CALCIUM AND INTEGRIN BINDING PROTEIN CIB - HOMO SAPIENS (HUMAN), 191 aa.	1.50E-96	
1141	cg43943478	408	AGGCTGCACAG CGCCACTCCAG GCT[G/gap]GGCC AGCTTGGCCCG CACTGGCAAC	G	gap			SILENT-NONCODING	cadherin	Human Gene Similar to SPTREMBL-ID:Q99971 CALCIUM AND INTEGRIN BINDING PROTEIN CIB - HOMO SAPIENS (HUMAN), 191 aa.	1.50E-96	

1142	cg43943478	410	GCTGCACAGCG CCACTCCAGGCT GG[G/gap]CCAGC TTGGCCCGCACT GGCAACAC	G	gap		SILENT-NONCODING	cadherin	Human Gene Similar to SPTREMBL-ID:Q99971 CALCIUM AND INTEGRIN BINDING PROTEIN CIB - HOMO SAPIENS (HUMAN), 191 aa.	1.50E-96	
1143	cg42924171	1026	CCCAACTTCCCC TGGAGCTCAGAG G[T/G]GTCCCCA CTGTACCAGCCT CTGATA	T	G		SILENT-NONCODING	calcium_channel	Human Gene Homologous to SWISSPROT-ID:Q06432 DIHYDROPYRIDINE-SENSITIVE L-TYPE, SKELETAL MUSCLE CALCIUM CHANNEL GAMMA SUBUNIT - HOMO SAPIENS (HUMAN), 222 aa.	7.30E-120	17
1144	cg42924171	1028	CAACTTCCCCTG GAGCTCAGAGGT G[T/G]CCCCACT GTACCAGCCTCT GATAAG	T	G		SILENT-NONCODING	calcium_channel	Human Gene Homologous to SWISSPROT-ID:Q06432 DIHYDROPYRIDINE-SENSITIVE L-TYPE, SKELETAL MUSCLE CALCIUM CHANNEL GAMMA SUBUNIT - HOMO SAPIENS (HUMAN), 222 aa.	7.30E-120	17
1145	cg42924171	1160	TCTCTTTCTCGG TGATAAAACACA C[C/G]CGCTCCG GTGAGCCCAGC GTCCCCT	C	G		SILENT-NONCODING	calcium_channel	Human Gene Homologous to SWISSPROT-ID:Q06432 DIHYDROPYRIDINE-SENSITIVE L-TYPE, SKELETAL MUSCLE CALCIUM CHANNEL GAMMA SUBUNIT - HOMO SAPIENS (HUMAN), 222 aa.	7.30E-120	17
1146	cg42924171	1169	CGGTGATAAAAC ACACCCGCTCCG G[T/gap]GAGCCC AGCGTCCCCTCC TTGGCTT	T	gap		SILENT-NONCODING	calcium_channel	Human Gene Homologous to SWISSPROT-ID:Q06432 DIHYDROPYRIDINE-SENSITIVE L-TYPE, SKELETAL MUSCLE CALCIUM CHANNEL GAMMA SUBUNIT - HOMO SAPIENS (HUMAN), 222 aa.	7.30E-120	17
1147	cg42924171	1177	AACACACCCGCT CCGGTGAGCCC AG[gap/G]CGTCC CCTCCTTGGCTT CCAGGAGC	gap	G		SILENT-NONCODING	calcium_channel	Human Gene Homologous to SWISSPROT-ID:Q06432 DIHYDROPYRIDINE-SENSITIVE L-TYPE, SKELETAL MUSCLE CALCIUM CHANNEL GAMMA SUBUNIT - HOMO SAPIENS (HUMAN), 222 aa.	7.30E-120	17

1148	cg42924171	1179	ACACACCCGCTC CGGTGAGCCCA GC[G/C]TCCCCT CCTTGGCTTCCA GGAGCCC	G	C		SILENT-NONCODING	calcium_channel	Human Gene Homologous to SWISSPROT-ID:Q06432 DIHYDROPYRIDINE-SENSITIVE L-TYPE, SKELETAL MUSCLE CALCIUM CHANNEL GAMMA SUBUNIT - HOMO SAPIENS (HUMAN), 222 aa.	7.30E-120	17
1149	cg42924171	1184	CCGCTCCGGTG AGCCCAGCGTC CCC[gap/C]TCCT TGGCTTCCAGGA GCCCTGGGA	gap	C		SILENT-NONCODING	calcium_channel	Human Gene Homologous to SWISSPROT-ID:Q06432 DIHYDROPYRIDINE-SENSITIVE L-TYPE, SKELETAL MUSCLE CALCIUM CHANNEL GAMMA SUBUNIT - HOMO SAPIENS (HUMAN), 222 aa.	7.30E-120	17
1150	cg42924171	1204	GTCCCCTCCTTG GCTTCCAGGAGC C[C/gap]TGGGAA GCATTTTTAACT GGGTAGA	C	gap		SILENT-NONCODING	calcium_channel	Human Gene Homologous to SWISSPROT-ID:Q06432 DIHYDROPYRIDINE-SENSITIVE L-TYPE, SKELETAL MUSCLE CALCIUM CHANNEL GAMMA SUBUNIT - HOMO SAPIENS (HUMAN), 222 aa.	7.30E-120	17
1151	cg42924171	1208	CCTCCTTGGCTT CCAGGAGCCCT GG[G/gap]AAGCA TTTTTAACTGGG TAGAATCT	G	gap		SILENT-NONCODING	calcium_channel	Human Gene Homologous to SWISSPROT-ID:Q06432 DIHYDROPYRIDINE-SENSITIVE L-TYPE, SKELETAL MUSCLE CALCIUM CHANNEL GAMMA SUBUNIT - HOMO SAPIENS (HUMAN), 222 aa.	7.30E-120	17
1152	cg42924171	746	ATGCTGAGCCCG AGCACTAACCCT C[C/gap]TGCGGC CCTAGCGACCCT CAGGCTT	C	gap		SILENT-NONCODING	calcium_channel	Human Gene Homologous to SWISSPROT-ID:Q06432 DIHYDROPYRIDINE-SENSITIVE L-TYPE, SKELETAL MUSCLE CALCIUM CHANNEL GAMMA SUBUNIT - HOMO SAPIENS (HUMAN), 222 aa.	7.30E-120	17
1153	cg42924171	868	GCTCCCATCTGC CCCCCTGCAACA G[T/C]CGCAGGC TGCTTCCTCTCT CTGAGT	T	C		SILENT-NONCODING	calcium_channel	Human Gene Homologous to SWISSPROT-ID:Q06432 DIHYDROPYRIDINE-SENSITIVE L-TYPE, SKELETAL MUSCLE CALCIUM CHANNEL GAMMA SUBUNIT - HOMO SAPIENS (HUMAN), 222 aa.	7.30E-120	17

1154	cg42924171	869	CTCCCATCTGCCCCCCTGCAACAGT[C/T]GCAGGCTGCTTCCTCTCTCTGAGTT	C	T			SILENT-NONCODING	calcium_channel	Human Gene Homologous to SWISSPROT-ID:Q06432 DIHYDROPYRIDINE-SENSITIVE L-TYPE, SKELETAL MUSCLE CALCIUM CHANNEL GAMMA SUBUNIT - HOMO SAPIENS (HUMAN), 222 aa.	7.30E-120	17
1155	cg42924171	907	CTCTCTCTGAGTTCCTCTGGGCTGC[C/gap]GCAGGCTCCCCCTGGGAATAGAGCAA	C	gap			SILENT-NONCODING	calcium_channel	Human Gene Homologous to SWISSPROT-ID:Q06432 DIHYDROPYRIDINE-SENSITIVE L-TYPE, SKELETAL MUSCLE CALCIUM CHANNEL GAMMA SUBUNIT - HOMO SAPIENS (HUMAN), 222 aa.	7.30E-120	17
1156	cg42924171	958	GACGTGAGTCCTAACCTGGCCACAG[C/T]TGGGGGACAGGCAGAGCCAGGTGG	C	T			SILENT-NONCODING	calcium_channel	Human Gene Homologous to SWISSPROT-ID:Q06432 DIHYDROPYRIDINE-SENSITIVE L-TYPE, SKELETAL MUSCLE CALCIUM CHANNEL GAMMA SUBUNIT - HOMO SAPIENS (HUMAN), 222 aa.	7.30E-120	17
1157	cg42924171	967	CCTAACCTGGCCACAGCTGGGGGAG[G/gap]CAGAGCCAGCAGGTGGACAGGTGTT	G	gap			SILENT-NONCODING	calcium_channel	Human Gene Homologous to SWISSPROT-ID:Q06432 DIHYDROPYRIDINE-SENSITIVE L-TYPE, SKELETAL MUSCLE CALCIUM CHANNEL GAMMA SUBUNIT - HOMO SAPIENS (HUMAN), 222 aa.	7.30E-120	17
1158	cg43246381	243	ACCTGGATTTGTTTTCAGCTTTCTC[G/A]ATTTTCACATGCACGTTAGGCTATC	G	A			SILENT-NONCODING	calcium_channel	Human Gene Similar to TREMBLNEW-ID:G259184 RYANODINE RECEPTOR/CALCIUM RELEASE CHANNEL - ORYCTOLAGUS SP, 4872 aa.	1.00E-73	12
1159	cg43933897	195	TCAGATGCCAGCTCTCCTCAGCGG A[C/gap]GCTCCTGATCCCTCAATTTGCCATC	C	gap			SILENT-NONCODING	calcium_channel	Human Gene Similar to TREMBLNEW-ID:G259184 RYANODINE RECEPTOR/CALCIUM RELEASE CHANNEL - ORYCTOLAGUS SP, 4872 aa.	9.70E-66	

1160	cg43919581	2171	AGGAATGCCTCC TCCCTGGGCAGA A[A/gap]GTGGCC ATGCCACCCTGT TTTCAGC	A	gap			SILENT-NONCODING	cathepsin	Human Gene SWISSPROT-ID:P00750 TISSUE PLASMINOGEN ACTIVATOR PRECURSOR (EC 3.4.21.68) (TPA) (T-PLASMINOGEN ACTIVATOR) - HOMO SAPIENS (HUMAN), 562 aa.	0.00E+00	8 (8p12)
1161	cg43919581	2357	TATAGTCACAAG AGCCCAGCAGG GC[C/gap]TCAAA GTTGGGGCAGG CTGGCTGGC	C	gap			SILENT-NONCODING	cathepsin	Human Gene SWISSPROT-ID:P00750 TISSUE PLASMINOGEN ACTIVATOR PRECURSOR (EC 3.4.21.68) (TPA) (T-PLASMINOGEN ACTIVATOR) - HOMO SAPIENS (HUMAN), 562 aa.	0.00E+00	8 (8p12)
1162	cg43946028	394	GAATCTCGTGCC TCAGCCTCCCAA G[T/C]AGCTGGG ATTACAGGCATG CACCAC	T	C			SILENT-NONCODING	cathepsin	Human Gene SWISSPROT-ID:P25774 CATHEPSIN S PRECURSOR (EC 3.4.22.27) - HOMO SAPIENS (HUMAN), 331 aa.	3.10E-185	
1163	cg43946028	403	GCCTCAGCCTCC CAAGTAGCTGGG A[T/C]TACAGGCA TGCACCACCGTG CTCGG	T	C			SILENT-NONCODING	cathepsin	Human Gene SWISSPROT-ID:P25774 CATHEPSIN S PRECURSOR (EC 3.4.22.27) - HOMO SAPIENS (HUMAN), 331 aa.	3.10E-185	
1164	cg43946028	468	TTTTAGTAGAGA TGGGGTTTCACC A[T/C]GTTAGCCA GGCTGCTCTTTA ACTCC	T	C			SILENT-NONCODING	cathepsin	Human Gene SWISSPROT-ID:P25774 CATHEPSIN S PRECURSOR (EC 3.4.22.27) - HOMO SAPIENS (HUMAN), 331 aa.	3.10E-185	
1165	cg43264626	197	ATAGACATTTCT ACCTTGAGGATA T[A/T]GAAGGGAA CTTAGGAAGTGA GAAGT	A	T			SILENT-NONCODING	cathepsin	Human Gene SWISSPROT-ID:P43235 CATHEPSIN K PRECURSOR (EC 3.4.22.38) (CATHESPIN O) (CATHEPSIN X) (CATHEPSIN O2) - HOMO SAPIENS (HUMAN), 329 aa.	4.10E-183	1
1166	cg43264626	41	TTTGAATGTGTA CTAGATGCTATT T[A/T]TTAAACTG TAGACAGGAGAT AAATA	A	T			SILENT-NONCODING	cathepsin	Human Gene SWISSPROT-ID:P43235 CATHEPSIN K PRECURSOR (EC 3.4.22.38) (CATHESPIN O) (CATHEPSIN X) (CATHEPSIN O2) - HOMO SAPIENS (HUMAN), 329 aa.	4.1E-183	1

1167	cg43264626	437	TGAAAAAGGTCATGGGTGGAGAGAA[G/C]CAAAGTAGGAAGGATCATTTGAAGC	G	C			SILENT-NONCODING	cathepsin	Human Gene SWISSPROT-ID:P43235 CATHEPSIN K PRECURSOR (EC 3.4.22.38) (CATHESPIN O) (CATHEPSIN X) (CATHEPSIN O2) - HOMO SAPIENS (HUMAN), 329 aa.	4.1E-183	1
1168	cg42926989	826	TCTTCGGTTCCTACGACCCCCGAAG[G/gap]CAGATTTGTGTGGGGGACCGGCGGG	G	gap			SILENT-NONCODING	cathepsin	Human Gene Homologous to SWISSPROT-ID:P08311 CATHEPSIN G PRECURSOR (EC 3.4.21.20) - HOMO SAPIENS (HUMAN), 255 aa.	1.7E-136	14 (14q11.2)
1169	cg42926989	908	AGGCCCCCTGCTGTGTAACAATGTG[G/gap]CCCACGGCATCGTCTCCTATGGAAA	G	gap			SILENT-NONCODING	cathepsin	Human Gene Homologous to SWISSPROT-ID:P08311 CATHEPSIN G PRECURSOR (EC 3.4.21.20) - HOMO SAPIENS (HUMAN), 255 aa.	1.7E-136	14 (14q11.2)
1170	cg42094318	1232	CCAACCCCTGAGCACCCCTATCAAC[C/T]CCCTATTGTAGTAAACTTGGAACCT	C	T			SILENT-NONCODING	cathepsin	Human Gene Homologous to SWISSPROT-ID:P20151 GLANDULAR KALLIKREIN 2 PRECURSOR (EC 3.4.21.35) (TISSUE KALLIKREIN) (PROSTATE) (HGK-1) - HOMO SAPIENS (HUMAN), 261 aa.	5.5E-110	19 (19q13)
1171	cg43982945	461	ACACATGTCAGGCTGGGGCAGCAGC[C/gap]ACTCTGATCAGCACCAGGTCCCGAG	C	gap			SILENT-NONCODING	cathepsin	Human Gene Similar to SWISSPROT-ID:Q26534 CATHEPSIN L PRECURSOR (EC 3.4.22.15) (SMCL1) - SCHISTOSOMA MANSONI (BLOOD FLUKE), 319 aa.	2E-80	11
1172	cg43982945	97	GGTTACAAGTTTCCTGGACATGGAG[A/G]GGGACACTATCCCTAAATCCAAGGG	A	G			SILENT-NONCODING	cathepsin	Human Gene Similar to SWISSPROT-ID:Q26534 CATHEPSIN L PRECURSOR (EC 3.4.22.15) (SMCL1) - SCHISTOSOMA MANSONI (BLOOD FLUKE), 319 aa.	2E-80	11
1173	cg43925458	591	TCTGGACATAAATCTGCCATTTATT[A/G]AACCATTCACTACAACAAATAAATA	A	G			SILENT-NONCODING	cathepsin inhib	Human Gene SWISSPROT-ID:P20810 CALPAIN INHIBITOR (CALPASTATIN) (SPERM BS-17 COMPONENT) - HOMO SAPIENS (HUMAN), 708 aa.	0	5 (5q15)

1174	cg43980411	1763	AGTAGGTATCCC TCCATGCCCTTC T[G/A]TAATAAAT ATCTGGAAAAAA CATTA	G	A			SILENT-NONCODING	cathepsin inhib	Human Gene SWISSPROT-ID:P05120 PLASMINOGEN ACTIVATOR INHIBITOR-2, PLACENTAL (PAI-2) (MONOCYTE ARG- SERPIN) (UROKINASE INHIBITOR) - HOMO SAPIENS (HUMAN), 415 aa.	3.2E-222	18 (18q21.3)
1175	cg43971453	1029	CTGTAGCTGCCT CCTGCCTTCCGA A[G/gap]GCAGAA GGAATGAAAGAT GCACATT	G	gap			SILENT-NONCODING	chloride_channel	Human Gene SWISSPROT-ID:P51788 CHLORIDE CHANNEL PROTEIN 2 (CLC 2) - HOMO SAPIENS (HUMAN), 898 aa.	0	3
1176	cg43971453	536	GGGTGTTAATGC CCACGTAGTGGA G[G/gap]CCTCTG GCAGATCCTGCA TTCCAAG	G	gap			SILENT-NONCODING	chloride_channel	Human Gene SWISSPROT-ID:P51788 CHLORIDE CHANNEL PROTEIN 2 (CLC 2) - HOMO SAPIENS (HUMAN), 898 aa.	0	3
1177	cg43971453	885	CCCCAACCCATC CTGCCAGGGCA GG[G/gap]CCTAT CTTCCTGCCTCT GGAAGACT	G	gap			SILENT-NONCODING	chloride_channel	Human Gene SWISSPROT-ID:P51788 CHLORIDE CHANNEL PROTEIN 2 (CLC 2) - HOMO SAPIENS (HUMAN), 898 aa.	0.00E+00	3
1178	cg43970982	5505	GACCAATGCCTT AATTAAAGAATTT [A/T]AAAAAGTTG TAATAGAGAATA TTTT	A	T			SILENT-NONCODING	collagen	Human Gene SWISSPROT-ID:P12111 COLLAGEN ALPHA 3(VI) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 3176 aa.	0.00E+00	2
1179	cg43970982	5564	CTCTAATGTTGT GTGTTTTTTTTTT [T/G]TGTGTGCTG GAGGGAGGGGA TTTAA	T	G			SILENT-NONCODING	collagen	Human Gene SWISSPROT-ID:P12111 COLLAGEN ALPHA 3(VI) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 3176 aa.	0.00E+00	2
1180	cg42201364	2443	TTAAAAACAAAC AACAAAAAACAA A[gap/G]CAACAA AAAAAAAAATTAA AAAAAA	gap	G			SILENT-NONCODING	collagen	Human Gene SWISSPROT-ID:Q03692 COLLAGEN ALPHA 1(X) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 680 aa.	0.00E+00	6

1181	cg42201364	2818	GCTTTCATCAAT GAACCTTTTCAA A[gap/A]CTTTTCT ATGATTGCAGAG AAGCTT	gap	A			SILENT-NONCODING	collagen	Human Gene SWISSPROT-ID:Q03692 COLLAGEN ALPHA 1(X) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 680 aa.	0.00E+00	6
1182	cg42201364	3169	GTTTTACCTACT CCTTATTTACGA C[A/G]CAATAAAA TAACATCAATAG AATTT	A	G			SILENT-NONCODING	collagen	Human Gene SWISSPROT-ID:Q03692 COLLAGEN ALPHA 1(X) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 680 aa.	0.00E+00	6
1183	cg42201364	3191	GACACAATAAAA TAACATCAATAG A[A/T]TTTTAGGC TGAATTAATTTGA AAGC	A	T			SILENT-NONCODING	collagen	Human Gene SWISSPROT-ID:Q03692 COLLAGEN ALPHA 1(X) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 680 aa.	0.00E+00	6
1184	cg41035069	3660	GCTTTTTTTTTTT TTTTTTTTTTTT[T/gap]GGGAGTAAG CCAGGCATTAAA AGCA	T	gap			SILENT-NONCODING	collagen	Human Gene TREMBLNEW-ID:D1024188 TYPE XIX COLLAGEN A1 CHAIN - HOMO SAPIENS (HUMAN), 1143 aa.	0.00E+00	6 (6q12)
1185	cg43917054	12431	ACCGTCTTGATC GGAAAGCTCTTC C[T/G]AATCGCTA ATCAGTCATTTC TTCAT	T	G			SILENT-NONCODING	collagen	Human Gene SWISSPROT-ID:Q14031 COLLAGEN ALPHA 6(IV) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 1678 aa.	0.00E+00	X (Xq22)
1186	cg43917054	12851	GAGGATGCAACA AATGTGGCCAAG C[C/gap]TATCAA AGGAAATGAGAA TGACAGC	C	gap			SILENT-NONCODING	collagen	Human Gene SWISSPROT-ID:Q14031 COLLAGEN ALPHA 6(IV) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 1678 aa.	0.00E+00	X (Xq22)
1187	cg43917054	12916	CAGAAGTAGAGG GGGTGGGTGCG TA[A/gap]GGATG TGTGAGTTTTGC TTTTGACT	A	gap			SILENT-NONCODING	collagen	Human Gene SWISSPROT-ID:Q14031 COLLAGEN ALPHA 6(IV) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 1678 aa.	0.00E+00	X (Xq22)

1188	cg43917054	13001	TCTCAGAAGTCC CTGTTTATTCCA A[A/T]TGCCATCC AGATGTGTGCAA TGTGG	A	T			SILENT-NONCODING	collagen	Human Gene SWISSPROT-ID:Q14031 COLLAGEN ALPHA 6(IV) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 1678 aa.	0.00E+00	X (Xq22)
1189	cg43917054	13009	GTCCCTGTTTAT TCCAAATGCCAT C[C/gap]AGATGT GTGCAATGTGGC AAACTGA	C	gap			SILENT-NONCODING	collagen	Human Gene SWISSPROT-ID:Q14031 COLLAGEN ALPHA 6(IV) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 1678 aa.	0.00E+00	X (Xq22)
1190	cg42740351	1046	TGAAGCTAAAAA AGACAGCAGAAC T[G/C]GTATTTTT CATCCTAAAGAA CAAAG	G	C			SILENT-NONCODING	collagen	Human Gene SWISSPROT-ID:Q28084 COLLAGEN ALPHA 3(IV) CHAIN - BOS TAURUS (BOVINE), 471 aa (fragment).	6.80E-174	2 (2q36)
1191	cg42740351	1047	GAAGCTAAAAAA GACAGCAGAACT G[G/C]TATTTTTC ATCCTAAAGAAC AAAGT	G	C			SILENT-NONCODING	collagen	Human Gene SWISSPROT-ID:Q28084 COLLAGEN ALPHA 3(IV) CHAIN - BOS TAURUS (BOVINE), 471 aa (fragment).	6.80E-174	2 (2q36)
1192	cg42740351	1131	CTTTAACCAAAC AATATTGCTCCA T[G/C]ATGACTTA GTACAAAGTTTC AATTT	G	C			SILENT-NONCODING	collagen	Human Gene SWISSPROT-ID:Q28084 COLLAGEN ALPHA 3(IV) CHAIN - BOS TAURUS (BOVINE), 471 aa (fragment).	6.80E-174	2 (2q36)
1193	cg43968268	20	TTTTAAATATATA CAAAGG[A/C]ATT TTATTATTAACCA AAGAAAGGG	A	C			SILENT-NONCODING	collagen	Human Gene Homologous to SPTREMBL-ID:Q61429 TYPE III COLLAGEN - MUS MUSCULUS (MOUSE), 1464 aa.	8.20E-128	1 (1p21)
1194	cg43991318	328	AACAGCAATTAA AAACAACAACAA C[A/gap]ACAAAA AAAAACATTCAC AACCTGT	A	gap			SILENT-NONCODING	collagen	Human Gene Similar to SWISSPROT-ID:Q07092 COLLAGEN ALPHA 1(XVI) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 1603 aa.	1.30E-73	1 (1p34)

1195	cg43991318	339	AAAACAACAACA ACAACAAAAAAA A[A/gap]CATTCA CAACCTGTCACA GAGTCCT	A	gap			SILENT-NONCODING	collagen	Human Gene Similar to SWISSPROT-ID:Q07092 COLLAGEN ALPHA 1(XVI) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 1603 aa.	1.30E-73	1 (1p34)
1196	cg43938820	487	TCTGCGGGAGG GAGGAGCAGAC GGG[G/gap]TTAG CACCGTTAATCT CGAGGGTCT	G	gap			SILENT-NONCODING	collagen	Human Gene Similar to SPTREMBL-ID:Q14040 ALPHA-1 COLLAGEN VI (AA 574-1009) - HOMO SAPIENS (HUMAN), 436 aa (fragment).	5.00E-59	21 (21q22.3)
1197	cg43938820	862	GGGCGTCTTGCT CAGGCTGGTGG GA[T/C]GCAGCA CAGAGGTGCCTA GGGAAGG	T	C			SILENT-NONCODING	collagen	Human Gene Similar to SPTREMBL-ID:Q14040 ALPHA-1 COLLAGEN VI (AA 574-1009) - HOMO SAPIENS (HUMAN), 436 aa (fragment).	5.00E-59	21 (21q22.3)
1198	cg39659519	2155	GTGTGTATGTGT GCGTGTGTGTAT G[C/T]GTGCATGT GTGTGTGTGTGT GTGTG	C	T			SILENT-NONCODING	collagen	Human Gene Similar to SWISSPROT-ID:Q99715 COLLAGEN ALPHA 1(XII) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 3063 aa.\|pcls:SPTREMBL-ID:Q99715 COLLAGEN TYPE XII ALPHA 1 PRECURSOR - HOMO SAPIENS (HUMAN), 3063 aa.	4.10E-52	1 (1p35)
1199	cg43278293	369	TTTCCTGCCTCT GCCTTGACCCGA A[G/gap]GTCTTA CAGGAAGACAAT AAATAAA	G	gap			SILENT-NONCODING	collagen	Human Gene Similar to SPTREMBL-ID:Q14058 PRO ALPHA 1(II) COLLAGEN - HOMO SAPIENS (HUMAN), 288 aa (fragment).	6.50E-50	12 (12q13.11)
1200	cg43278293	370	TTCCTGCCTCTG CCTTGACCCGAA G[G/gap]TCTTAC AGGAAGACAATA AATAAAT	G	gap			SILENT-NONCODING	collagen	Human Gene Similar to SPTREMBL-ID:Q14058 PRO ALPHA 1(II) COLLAGEN - HOMO SAPIENS (HUMAN), 288 aa (fragment).	6.50E-50	12 (12q13.11)

1201	cg43063256	2090	AGAGCCCTGAGCCCTCAAGAACTCA[C/T]GCCAGCTCAGCCCTACACCAGTTTC	C	T			SILENT-NONCODING	complement	Human Gene SWISSNEW-ID:P07358 COMPLEMENT COMPONENT C8 BETA CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 591 aa.\|pcls:SWISSPROT-ID:P07358 COMPLEMENT COMPONENT C8 BETA CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 591 aa.	0.00E+00	1 (1p32)
1202	cg43281450	229	AATCCTCAGAAGAAAGAAAGGGGCC[C/gap]TTTGGGTTGTTTCAGGTAAAGTACA	C	gap			SILENT-NONCODING	complement	Human Gene SWISSPROT-ID:P00736 COMPLEMENT C1R COMPONENT PRECURSOR (EC 3.4.21.41) - HOMO SAPIENS (HUMAN), 705 aa.	0.00E+00	12 (12p13)
1203	cg43281450	368	GTCAGTTGTTTTTTGTTTTTTTTTT[T/gap]CCACACTGCTCTCTGGATTCGAACC	T	gap			SILENT-NONCODING	complement	Human Gene SWISSPROT-ID:P00736 COMPLEMENT C1R COMPONENT PRECURSOR (EC 3.4.21.41) - HOMO SAPIENS (HUMAN), 705 aa.	0.00E+00	12 (12p13)
1204	cg43281450	368	TCAGTTGTTTTTTGTTTTTTTTTT[gap/T]CCACACTGCTCTCTGGATTCGAACC	gap	T			SILENT-NONCODING	complement	Human Gene SWISSPROT-ID:P00736 COMPLEMENT C1R COMPONENT PRECURSOR (EC 3.4.21.41) - HOMO SAPIENS (HUMAN), 705 aa.	0.00E+00	12 (12p13)
1205	cg43049885	3106	CTCAAAGTTACTGACAAAAATTATT[T/C]TCTGTTAGTTTGAGATCATTATTCT	T	C			SILENT-NONCODING	complement	Human Gene TREMBLNEW-ID:G386348 COMPLEMENT C6 - HOMO SAPIENS, 941 aa.	0.00E+00	5 (5p13)
1206	cg43049885	3303	GTAGCCTGTGACATTAAGCATTCTC[A/G]CAATTAGAAATAAGAATAAAACCCA	A	G			SILENT-NONCODING	complement	Human Gene TREMBLNEW-ID:G386348 COMPLEMENT C6 - HOMO SAPIENS, 941 aa.	0.00E+00	5 (5p13)
1207	cg43933757	3223	GTTCAAGCGATTCTTGTGCCTCAGC[C/T]TCCCAAGCAGCTGGGATTACAGGTG	C	T			SILENT-NONCODING	complement	Human Gene SWISSPROT-ID:P10643 COMPLEMENT COMPONENT C7 PRECURSOR - HOMO SAPIENS (HUMAN), 843 aa.	0.00E+00	5 (5p13)

1208	cg43958722	254	GAAACCAGCCTGGGCAACATAGGAA[A/G]ATCCTGTCTCTACAAAAAATAAATT	A	G			SILENT-NONCODING	complement	Human Gene SWISSPROT-ID:P08174 COMPLEMENT DECAY-ACCELERATING FACTOR PRECURSOR (CD55) - HOMO SAPIENS (HUMAN), 381 aa.	3.40E-192	1 (1q32)
1209	cg43958722	287	CTCTACAAAAAATAAATTTCAAAAA[C/gap]TTAGCCGGGTGTCGTGGCACACACC	C	gap			SILENT-NONCODING	complement	Human Gene SWISSPROT-ID:P08174 COMPLEMENT DECAY-ACCELERATING FACTOR PRECURSOR (CD55) - HOMO SAPIENS (HUMAN), 381 aa.	3.40E-192	1 (1q32)
1210	cg43956185	308	TTTTGGAGTTTTTTAGTTTTCCAAG[T/A]TTTAATATGGTGCTTTTAAGAAGAG	T	A			SILENT-NONCODING	complement	Human Gene SWISSPROT-ID:Q03591 COMPLEMENT FACTOR H-LIKE PROTEIN 1 PRECURSOR (H36) - HOMO SAPIENS (HUMAN), 330 aa.	4.10E-190	1
1211	cg43956185	423	AAAGGAGTAAAACAATACTTAAAAA[T/A]TAAATTAAGAACTGATTTAATACTA	T	A			SILENT-NONCODING	complement	Human Gene SWISSPROT-ID:Q03591 COMPLEMENT FACTOR H-LIKE PROTEIN 1 PRECURSOR (H36) - HOMO SAPIENS (HUMAN), 330 aa.	4.10E-190	1
1212	cg43956185	430	TAAAACAATACTTAAAAATTAAATT[A/G]AGAACTGATTTAATACTAAAGTTCT	A	G			SILENT-NONCODING	complement	Human Gene SWISSPROT-ID:Q03591 COMPLEMENT FACTOR H-LIKE PROTEIN 1 PRECURSOR (H36) - HOMO SAPIENS (HUMAN), 330 aa.	4.10E-190	1
1213	cg43956185	471	CTAAAGTTCTGAATAAAGGTGTGCA[T/C]TTTATGATTGATTCTATCTTTTTGC	T	C			SILENT-NONCODING	complement	Human Gene SWISSPROT-ID:Q03591 COMPLEMENT FACTOR H-LIKE PROTEIN 1 PRECURSOR (H36) - HOMO SAPIENS (HUMAN), 330 aa.	4.1E-190	1
1214	cg43945714	1056	TACCCCCAACACCACCCCTTGCCCA[G/A]CCAATGCACACAGTAGGGCTTGGTG	G	A			SILENT-NONCODING	complement	Human Gene Homologous to SWISSPROT-ID:P02746 COMPLEMENT C1Q SUBCOMPONENT, B CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 251 aa.	3.5E-138	1 (1p36.3)

1215	cg43945714	1063	AACACCACCCCT TGCCCAGCCAAT G[C/G]ACACAGT AGGGCTTGGTGA ATGCTG	C	G			SILENT-NONCODING	complement	Human Gene Homologous to SWISSPROT-ID:P02746 COMPLEMENT C1Q SUBCOMPONENT, B CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 251 aa.	3.5E-138	1 (1p36.3)
1216	cg43945714	1124	GAGTAAATAAAC TCTTCAAGGCCA A[G/A]GAACAGT GGTCTAATTCAA CTCTGT	G	A			SILENT-NONCODING	complement	Human Gene Homologous to SWISSPROT-ID:P02746 COMPLEMENT C1Q SUBCOMPONENT, B CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 251 aa.	3.5E-138	1 (1p36.3)
1217	cg43945714	1125	AGTAAATAAACT CTTCAAGGCCAA G[G/A]AACAGTG GTCTAATTCAAC TCTGTG	G	A			SILENT-NONCODING	complement	Human Gene Homologous to SWISSPROT-ID:P02746 COMPLEMENT C1Q SUBCOMPONENT, B CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 251 aa.	3.5E-138	1 (1p36.3)
1218	cg43945714	1126	GTAAATAAACTC TTCAAGGCCAAG G[A/G]ACAGTGG TCTAATTCAACT CTGTGT	A	G			SILENT-NONCODING	complement	Human Gene Homologous to SWISSPROT-ID:P02746 COMPLEMENT C1Q SUBCOMPONENT, B CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 251 aa.	3.5E-138	1 (1p36.3)
1219	cg43945714	1160	CTAATTCAACTC TGTGTCCCAGCA C[C/gap]TGGCAC ACCAGAAGTGCC ATGCTCA	C	gap			SILENT-NONCODING	complement	Human Gene Homologous to SWISSPROT-ID:P02746 COMPLEMENT C1Q SUBCOMPONENT, B CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 251 aa.	3.5E-138	1 (1p36.3)

1220	cg43947909	969	CAGAAAAAAATG ATAATAAATGAG A[A/G]CACAAAAC ATATAATTTAAAT TTGG	A	G			SILENT-NONCODING	complement	Human Gene Homologous to SWISSPROT-ID:Q07021 COMPLEMENT COMPONENT 1, Q SUBCOMPONENT BINDING PROTEIN PRECURSOR (GLYCOPROTEIN GC1QBP) (GC1Q-R PROTEIN) (HYALURONAN-BINDING PROTEIN 1) (PRE-MRNA SPLICING FACTOR SF2, P32 SUBUNIT) - HOMO SAPIENS (HUMAN), 282 aa.	6.9E-129	17
1221	cg43947909	991	AGAACACAAAAC ATATAATTTAAAT [T/C]TGGTATTTT TTCCCCCATGAT ATTA	T	C			SILENT-NONCODING	complement	Human Gene Homologous to SWISSPROT-ID:Q07021 COMPLEMENT COMPONENT 1, Q SUBCOMPONENT BINDING PROTEIN PRECURSOR (GLYCOPROTEIN GC1QBP) (GC1Q-R PROTEIN) (HYALURONAN-BINDING PROTEIN 1) (PRE-MRNA SPLICING FACTOR SF2, P32 SUBUNIT) - HOMO SAPIENS (HUMAN), 282 aa.	6.9E-129	17
1222	cg43947909	326	ATTCAACAGGAG CTGATCAACCAA G[A/G]GCAGTCC ATCATCAGCGAG TATGAG	A	G			SILENT-NONCODING	complement	Human Gene Homologous to SWISSPROT-ID:Q07021 COMPLEMENT COMPONENT 1, Q SUBCOMPONENT BINDING PROTEIN PRECURSOR (GLYCOPROTEIN GC1QBP) (GC1Q-R PROTEIN) (HYALURONAN-BINDING PROTEIN 1) (PRE-MRNA SPLICING FACTOR SF2, P32 SUBUNIT) - HOMO SAPIENS (HUMAN), 282 aa.	6.9E-129	17

1223	cg43947909	575	ATAAATGAGCAC AGTGCACATTGT C[C/T]CCACACAC CTGAATTTTCAG TCACT	C	T			SILENT-NONCODING	complement	Human Gene Homologous to SWISSPROT-ID:Q07021 COMPLEMENT COMPONENT 1, Q SUBCOMPONENT BINDING PROTEIN PRECURSOR (GLYCOPROTEIN GC1QBP) (GC1Q-R PROTEIN) (HYALURONAN-BINDING PROTEIN 1) (PRE-MRNA SPLICING FACTOR SF2, P32 SUBUNIT) - HOMO SAPIENS (HUMAN), 282 aa.	6.9E-129	17
1224	cg43947909	839	ACATCTGTTCTT GGTCTTTTGTGA C[G/A]CAGGTTG AAGGGGGAGGA ATAGAAA	G	A			SILENT-NONCODING	complement	Human Gene Homologous to SWISSPROT-ID:Q07021 COMPLEMENT COMPONENT 1, Q SUBCOMPONENT BINDING PROTEIN PRECURSOR (GLYCOPROTEIN GC1QBP) (GC1Q-R PROTEIN) (HYALURONAN-BINDING PROTEIN 1) (PRE-MRNA SPLICING FACTOR SF2, P32 SUBUNIT) - HOMO SAPIENS (HUMAN), 282 aa.	6.9E-129	17
1225	cg43984382	141	CAGCCAGTCCTG GGGCTCTCAGA GC[C/gap]AGCCC CCTCCCTTCAGC AGCTGAAG	C	gap			SILENT-NONCODING	complement	Human Gene Homologous to SWISSPROT-ID:P02745 COMPLEMENT C1Q SUBCOMPONENT, A CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 245 aa.	8.8E-101	1
1226	cg43942011	2028	TTTTCTATGAAG AGCCCCAGATG GA[gap/A]GTTTTT GGGGGGTGCAT GGCCTGCT	gap	A			SILENT-NONCODING	complementrecept	Human Gene Similar to TREMBLNEW-ID:E246058 COMPLEMENT RECEPTOR 2 - MUS MUSCULUS (MOUSE), 651 aa (fragment).	1.10E-69	1 (1q32)
1227	cg44028879	1058	TCTTCAGTCAGA GCTCGCCCTGTA G[C/G]CTCTCTGT CTGTGCCCTCCC CTCCC	C	G			SILENT-NONCODING	csf	Human Gene SWISSPROT-ID:P09603 MACROPHAGE COLONY STIMULATING FACTOR-1 PRECURSOR (CSF-1) (MCSF) - HOMO SAPIENS (HUMAN), 554 aa.	7.80E-299	1 (1p21)

1228	cg44028879	1129	CTTCCCTCTTGGGAATGTCAAAGTG[C/G]AAGATGCAGAAACCTGGGCGAACAA	C	G			SILENT-NONCODING	csf	Human Gene SWISSPROT-ID:P09603 MACROPHAGE COLONY STIMULATING FACTOR-1 PRECURSOR (CSF-1) (MCSF) - HOMO SAPIENS (HUMAN), 554 aa.	7.80E-299	1 (1p21)
1229	cg44028879	119	AAATAGATATTTAAATGACTTTATA[T/A]AAAATAATTCACCACTTCCAAGTAT	T	A			SILENT-NONCODING	csf	Human Gene SWISSPROT-ID:P09603 MACROPHAGE COLONY STIMULATING FACTOR-1 PRECURSOR (CSF-1) (MCSF) - HOMO SAPIENS (HUMAN), 554 aa.	7.80E-299	1 (1p21)
1230	cg44028879	1152	TGCAAGATGCAGAAACCTGGGCGAA[C/G]AACACAGCCTAAAGACCGGCTCTGG	C	G			SILENT-NONCODING	csf	Human Gene SWISSPROT-ID:P09603 MACROPHAGE COLONY STIMULATING FACTOR-1 PRECURSOR (CSF-1) (MCSF) - HOMO SAPIENS (HUMAN), 554 aa.	7.80E-299	1 (1p21)
1231	cg44028879	1168	CTGGGCGAACAACACAGCCTAAAGA[C/G]CGGCTCTGGCTGGCGGCCCAGGAGG	C	G			SILENT-NONCODING	csf	Human Gene SWISSPROT-ID:P09603 MACROPHAGE COLONY STIMULATING FACTOR-1 PRECURSOR (CSF-1) (MCSF) - HOMO SAPIENS (HUMAN), 554 aa.	7.80E-299	1 (1p21)
1232	cg44028879	134	TGACTTTATATAAAATAATTCACCA[C/G]TTCCAAGTATAAAAACAAAATCTCA	C	G			SILENT-NONCODING	csf	Human Gene SWISSPROT-ID:P09603 MACROPHAGE COLONY STIMULATING FACTOR-1 PRECURSOR (CSF-1) (MCSF) - HOMO SAPIENS (HUMAN), 554 aa.	7.80E-299	1 (1p21)
1233	cg44028879	137	CTTTATATAAAATAATTCACCACTT[C/G]CAAGTATAAAAACAAAATCTCACAG	C	G			SILENT-NONCODING	csf	Human Gene SWISSPROT-ID:P09603 MACROPHAGE COLONY STIMULATING FACTOR-1 PRECURSOR (CSF-1) (MCSF) - HOMO SAPIENS (HUMAN), 554 aa.	7.80E-299	1 (1p21)
1234	cg44028879	183	CACAGTGCGTGAGCCAATGTCCTCT[C/G]TTGACTTCTCAGAGAACAGAAGGGG	C	G			SILENT-NONCODING	csf	Human Gene SWISSPROT-ID:P09603 MACROPHAGE COLONY STIMULATING FACTOR-1 PRECURSOR (CSF-1) (MCSF) - HOMO SAPIENS (HUMAN), 554 aa.	7.80E-299	1 (1p21)

1235	cg44028879	188	TGCGTGAGCCAA TGTCCTCTCTTG A[C/G]TTCTCAGA GAACAGAAGGG GTTCCT	C	G		SILENT-NONCODING	csf	Human Gene SWISSPROT-ID:P09603 MACROPHAGE COLONY STIMULATING FACTOR-1 PRECURSOR (CSF-1) (MCSF) - HOMO SAPIENS (HUMAN), 554 aa.	7.80E-299	1 (1p21)
1236	cg44028879	232	GGTTCCTGAGCA GGTAGCCTGGG GG[G/gap]ACACC AGAGGTGGCTCT GGGGCTCC	G	gap		SILENT-NONCODING	csf	Human Gene SWISSPROT-ID:P09603 MACROPHAGE COLONY STIMULATING FACTOR-1 PRECURSOR (CSF-1) (MCSF) - HOMO SAPIENS (HUMAN), 554 aa.	7.80E-299	1 (1p21)
1237	cg44028879	460	AGGCTAAGCCCC ATATGCAAGTTC A[C/G]TGCCCTTC CCTAAGCTGTCG GCATC	C	G		SILENT-NONCODING	csf	Human Gene SWISSPROT-ID:P09603 MACROPHAGE COLONY STIMULATING FACTOR-1 PRECURSOR (CSF-1) (MCSF) - HOMO SAPIENS (HUMAN), 554 aa.	7.80E-299	1 (1p21)
1238	cg44028879	679	GCTCGTTGCCTA GGCCTCAGAGC CA[C/G]CACCAC AGGCTGGCCAC AAAGTGGA	C	G		SILENT-NONCODING	csf	Human Gene SWISSPROT-ID:P09603 MACROPHAGE COLONY STIMULATING FACTOR-1 PRECURSOR (CSF-1) (MCSF) - HOMO SAPIENS (HUMAN), 554 aa.	7.80E-299	1 (1p21)
1239	cg42542496	1400	ACACTGCCGACA TCAGCATTGTCT C[G/A]TGTACAGC TCCCTTCCCTGC AGGGC	G	A		SILENT-NONCODING	csf	Human Gene SWISSPROT-ID:P40225 THROMBOPOIETIN PRECURSOR (MEGAKARYOCYTE COLONY STIMULATING FACTOR) (C-MPL LIGAND) (ML) (MEGAKARYOCYTE GROWTH AND DEVELOPMENT FACTOR) (MGDF) - HOMO SAPIENS (HUMAN), 353 aa.	1.20E-189	3 (3q26.3)
1240	cg42542496	1635	AGAAATTTGCAA CTCACTGATTCT C[T/A]ACATGCTC TTTTTCTGTGATA ACTC	T	A		SILENT-NONCODING	csf	Human Gene SWISSPROT-ID:P40225 THROMBOPOIETIN PRECURSOR (MEGAKARYOCYTE COLONY STIMULATING FACTOR) (C-MPL LIGAND) (ML) (MEGAKARYOCYTE GROWTH AND DEVELOPMENT FACTOR) (MGDF) - HOMO SAPIENS (HUMAN), 353 aa.	1.20E-189	3 (3q26.3)

1241	cg42542496	1668	CTTTTTCTGTGAT G AACTCTGCAAAG[G/A]CCTGGGCTG GCCTGGCAGTTG AACA	A		SILENT-NONCODING	csf	Human Gene SWISSPROT-ID:P40225 THROMBOPOIETIN PRECURSOR (MEGAKARYOCYTE COLONY STIMULATING FACTOR) (C-MPL LIGAND) (ML) (MEGAKARYOCYTE GROWTH AND DEVELOPMENT FACTOR) (MGDF) - HOMO SAPIENS (HUMAN), 353 aa.	1.20E-189	3 (3q26.3)	
1242	cg42542496	1728	ACTAACCTTGAG A TCAGAAAACAGA G[A/G]AAGGGTA ATTTCCTTTGCTT CAAAT	G		SILENT-NONCODING	csf	Human Gene SWISSPROT-ID:P40225 THROMBOPOIETIN PRECURSOR (MEGAKARYOCYTE COLONY STIMULATING FACTOR) (C-MPL LIGAND) (ML) (MEGAKARYOCYTE GROWTH AND DEVELOPMENT FACTOR) (MGDF) - HOMO SAPIENS (HUMAN), 353 aa.	1.20E-189	3 (3q26.3)	
1243	cg41533258	1246	GTTTGACTCCCG T AACATCACCGAC G[T/C]GTCTCCTG TTTTTCTGGGTG GCCTC	C		SILENT-NONCODING	csf	Human Gene Homologous to SWISSPROT-ID:P09919 GRANULOCYTE COLONY-STIMULATING FACTOR PRECURSOR (G-CSF) (PLURIPOIETIN) - HOMO SAPIENS (HUMAN), 207 aa.	1.50E-107	17 (17q11.2)	
1244	cg2752665	774	GGAGTGGCCTG C GACCTGCCCTG GGC[C/gap]ACAC TGACCCTGATAC AGGCATGGC	gap		SILENT-NONCODING	csf	Human Gene Similar to SWISSPROT-ID:P04141 GRANULOCYTE-MACROPHAGE COLONY-STIMULATING FACTOR PRECURSOR (GM-CSF) (COLONY-STIMULATING FACTOR) (CSF) - HOMO SAPIENS (HUMAN), 144 aa.	5.00E-75	5 (5q31.1)	
1245	cg43931046	2754	AACCTCTTCAAA A GAAATAGGAGCA A[A/gap]CCCCCA AGAGGCTTAATT TACCAAT	gap		SILENT-NONCODING	cyclin	Human Gene SPTREMBL-ID:P70413 CYCLIN D-INTERACTING MYB-LIKE PROTEIN - MUS MUSCULUS (MOUSE), 761 aa.	0.00E+00	7	
1246	cg43931046	3843	AATTGTATATTCA T GTTTAACAGAAA[T/A]AAAGAATAT TTGTCTTAAGAT GCA	A		SILENT-NONCODING	cyclin	Human Gene SPTREMBL-ID:P70413 CYCLIN D-INTERACTING MYB-LIKE PROTEIN - MUS MUSCULUS (MOUSE), 761 aa.	0.00E+00	7	

1247	cg43920512	101	TGGCCTGGGCTGCGACCGGGGAGCA[A/C]GACTATTCTTTGGCCGGGTCGGTGC	A	C			SILENT-NONCODING	cyclin	Human Gene SWISSPROT-ID:P20248 G2/MITOTIC-SPECIFIC CYCLIN A - HOMO SAPIENS (HUMAN), 432 aa.	4.10E-231	4 (4q27)
1248	cg43920512	103	GCCTGGGCTGCGACCGGGGAGCAAG[A/C]CTATTCTTTGGCCGGGTCGGTGCGA	A	C			SILENT-NONCODING	cyclin	Human Gene SWISSPROT-ID:P20248 G2/MITOTIC-SPECIFIC CYCLIN A - HOMO SAPIENS (HUMAN), 432 aa.	4.10E-231	4 (4q27)
1249	cg43920512	1574	GTGTACAGTTTTTAACTTAGGTTTT[gap/T]AATTTTACAATCATTTCTGAATACA	gap	T			SILENT-NONCODING	cyclin	Human Gene SWISSPROT-ID:P20248 G2/MITOTIC-SPECIFIC CYCLIN A - HOMO SAPIENS (HUMAN), 432 aa.	4.10E-231	4 (4q27)
1250	cg43920512	2224	GAATAAAAAATACCCAGGGTTCTTT[T/G]AATGGAATAAATATCCCTTTTAATA	T	G			SILENT-NONCODING	cyclin	Human Gene SWISSPROT-ID:P20248 G2/MITOTIC-SPECIFIC CYCLIN A - HOMO SAPIENS (HUMAN), 432 aa.	4.10E-231	4 (4q27)
1251	cg43920512	95	GTAGGCTGGCCTGGGCTGCGACCGG[G/C]GAGCAAGACTATTCTTTGGCCGGGT	G	C			SILENT-NONCODING	cyclin	Human Gene SWISSPROT-ID:P20248 G2/MITOTIC-SPECIFIC CYCLIN A - HOMO SAPIENS (HUMAN), 432 aa.	4.10E-231	4 (4q27)
1252	cg43920512	98	GGCTGGCCTGGGCTGCGACCGGGGA[G/C]CAAGACTATTCTTTGGCCGGGTCGG	G	C			SILENT-NONCODING	cyclin	Human Gene SWISSPROT-ID:P20248 G2/MITOTIC-SPECIFIC CYCLIN A - HOMO SAPIENS (HUMAN), 432 aa.	4.10E-231	4 (4q27)
1253	cg43927697	2010	AGCGGGGAGAAGCAGAACACCGGAG[G/gap]CCCGACCAGCCAAGGACCTACACCC	G	gap			SILENT-NONCODING	cyclin	Human Gene SWISSPROT-ID:P14635 G2/MITOTIC-SPECIFIC CYCLIN B1 - HOMO SAPIENS (HUMAN), 433 aa.	3.60E-230	5 (5q12)

1254	cg43927697	609	CAGTAATATGTA CAGATGGCACAT G[G/gap]TGCCAA TTTTATTTGTAAA TATAGT	G	gap			SILENT-NONCODING	cyclin	Human Gene SWISSPROT-ID:P14635 G2/MITOTIC-SPECIFIC CYCLIN B1 - HOMO SAPIENS (HUMAN), 433 aa.	3.60E-230	5 (5q12)
1255	cg43927697	620	CAGATGGCACAT GGTGCCAATTTT A[gap/G]TTTGTAA ATATAGTACTCC AACTCA	gap	G			SILENT-NONCODING	cyclin	Human Gene SWISSPROT-ID:P14635 G2/MITOTIC-SPECIFIC CYCLIN B1 - HOMO SAPIENS (HUMAN), 433 aa.	3.60E-230	5 (5q12)
1256	cg43927697	628	ACATGGTGCCAA TTTTATTTGTAAA [gap/G]TATAGTA CTCCAACTCAAG TTTACA	gap	G			SILENT-NONCODING	cyclin	Human Gene SWISSPROT-ID:P14635 G2/MITOTIC-SPECIFIC CYCLIN B1 - HOMO SAPIENS (HUMAN), 433 aa.	3.60E-230	5 (5q12)
1257	cg43957094	1145	CCAAACATTTAT AATCAAGAGATT T[gap/A]TAATCAA TTATGTACTAGA ATCATA	gap	A			SILENT-NONCODING	cyclin	Human Gene SWISSPROT-ID:P24863 G1/S-SPECIFIC CYCLIN C - HOMO SAPIENS (HUMAN), 303 aa.	7.90E-164	6
1258	cg43957094	1145	CCAAACATTTAT AATCAAGAGATT T[gap/A]TAATCAA TTATGTACTAGA ATCATA	gap	A			SILENT-NONCODING	cyclin	Human Gene SWISSPROT-ID:P24863 G1/S-SPECIFIC CYCLIN C - HOMO SAPIENS (HUMAN), 303 aa.	7.90E-164	6
1259	cg43957094	1184	ACTAGAATCATA TTAAAGAAAAAC T[T/gap]ATTTTGC AAAAATAAAATC ACTTTC	T	gap			SILENT-NONCODING	cyclin	Human Gene SWISSPROT-ID:P24863 G1/S-SPECIFIC CYCLIN C - HOMO SAPIENS (HUMAN), 303 aa.	7.90E-164	6
1260	cg43957094	1189	AATCATATTAAA GAAAAACTTATTT [T/gap]GCAAAAA TAAAATCACTTTC CAATA	T	gap			SILENT-NONCODING	cyclin	Human Gene SWISSPROT-ID:P24863 G1/S-SPECIFIC CYCLIN C - HOMO SAPIENS (HUMAN), 303 aa.	7.90E-164	6

1261	cg43957094	800	TAAAATACACTTTTAAATCAATATA[gap/C]GGTACTTGATTAATTTCCCTGAAAT	gap	C			SILENT-NONCODING	cyclin	Human Gene SWISSPROT-ID:P24863 G1/S-SPECIFIC CYCLIN C - HOMO SAPIENS (HUMAN), 303 aa.	7.90E-164	6
1262	cg43242733	1125	ACTGGATTATTACAGCACCAAAAAA[gap/A]CTTCTCTGAAGCCTTTCTCCACAAC	gap	A			SILENT-NONCODING	cyclin	Human Gene SWISSPROT-ID:P51959 G2/MITOTIC-SPECIFIC CYCLIN G1 - HOMO SAPIENS (HUMAN), 295 aa.	1.30E-154	5
1263	cg43242733	1205	TGGATTTAAGCTATGAAGCCTCAAA[A/gap]CATCACGAGATAAGCATGATGGTCT	A	gap			SILENT-NONCODING	cyclin	Human Gene SWISSPROT-ID:P51959 G2/MITOTIC-SPECIFIC CYCLIN G1 - HOMO SAPIENS (HUMAN), 295 aa.	1.30E-154	5
1264	cg43951588	138	AAGAGTTCTAAACCAATAAGAAAAA[G/A]GGCACAATGAAGCACACATCCCCAG	G	A			SILENT-NONCODING	cyclin	Human Gene Similar to SWISSPROT-ID:P37883 G2/MITOTIC-SPECIFIC CYCLIN B2 - MESOCRICETUS AURATUS (GOLDEN HAMSTER), 397 aa.	2.10E-92	15
1265	cg43969364	569	TTAACCAGGCGTGGGGCCTCATGCT[A/T]GCAGTTCCAGCCACTCCGGAGGCTG	A	T			SILENT-NONCODING	cyclin	Human Gene Similar to TREMBLNEW-ID:G2668505 PUTATIVE CYCLIN G1 INTERACTING PROTEIN - HOMO SAPIENS (HUMAN), 154 aa.	9.70E-67	7
1266	cg43996855	1221	TTTCTTCCATATAAACACAGCTTTC[C/gap]TTTTGCCGCAAGCATCTGATGACGA	C	gap			SILENT-NONCODING	cyto450	Human Gene SPTREMBL-ID:Q93089 DIOXIN-INDUCIBLE CYTOCHROME P450 (EC 1.14.14.1) - HOMO SAPIENS (HUMAN), 543 aa.	3.20E-293	2 (2p22)
1267	cg43996855	2882	ATGCATACTTTAAAATTCATGATAA[A/C]TCATGGAACCCCACTATACTCACTA	A	C			SILENT-NONCODING	cyto450	Human Gene SPTREMBL-ID:Q93089 DIOXIN-INDUCIBLE CYTOCHROME P450 (EC 1.14.14.1) - HOMO SAPIENS (HUMAN), 543 aa.	3.20E-293	2 (2p22)

1268	cg43143315	2383	GGTTACAAACCG TTTCAGGCCCTG C[C/gap]TACCAC ATTCACTGTTTG AATCTTT	C	gap			SILENT-NONCODING	cyto450	Human Gene SWISSNEW-ID:Q07973 CYTOCHROME P450-CC24 MITOCHONDRIAL PRECURSOR (EC 1.14.-.-) (P450- CC24) (VITAMIN D(3) 24-HYDROXYLASE) (1,25-DIHYDROXYVITAMIN D(3) 24-HYDROXYLASE) (24-OHASE) - HOMO SAPIENS (HUMAN), 513 aa.	pcls:SWISSPROT-ID:Q07973 CYTOCHROME P450-CC24 MITOCHONDRIAL PRECURSOR (EC 1.14.-.-) (P450- CC24) (VITAMIN D(3) 24-HYDROXYLASE) (1,25-DIHYDROXYVITAMIN D(3) 24-HYDROXYLASE) (24-OHASE) - HOMO SAPIENS (HUMAN), 513 aa	1.90E-279	20
1269	cg43143315	2717	CTAGTGATTCAC TGGGGCATTATT T[T/gap]GTTAGA GGACCTTAAAAT TGTTTAT	T	gap			SILENT-NONCODING	cyto450	Human Gene SWISSNEW-ID:Q07973 CYTOCHROME P450-CC24 MITOCHONDRIAL PRECURSOR (EC 1.14.-.-) (P450- CC24) (VITAMIN D(3) 24-HYDROXYLASE) (1,25-DIHYDROXYVITAMIN D(3) 24-HYDROXYLASE) (24-OHASE) - HOMO SAPIENS (HUMAN), 513 aa.	pcls:SWISSPROT-ID:Q07973 CYTOCHROME P450-CC24 MITOCHONDRIAL PRECURSOR (EC 1.14.-.-) (P450- CC24) (VITAMIN D(3) 24-HYDROXYLASE) (1,25-DIHYDROXYVITAMIN D(3) 24-HYDROXYLASE) (24-OHASE) - HOMO SAPIENS (HUMAN), 513 aa	1.90E-279	20

1270	cg43143315	2951	GATTTAGGATCTGTGGTGCAGGGCA[A/gap]TGTTTCAAAGTTTAGTCACAGCTTA	A	gap		SILENT-NONCODING	cyto450	Human Gene SWISSNEW-ID:Q07973 CYTOCHROME P450-CC24 MITOCHONDRIAL PRECURSOR (EC 1.14.-.-) (P450- CC24) (VITAMIN D(3) 24-HYDROXYLASE) (1,25-DIHYDROXYVITAMIN D(3) 24-HYDROXYLASE) (24-OHASE) - HOMO SAPIENS (HUMAN), 513 aa.	pcis:SWISSPROT-ID:Q07973 CYTOCHROME P450-CC24 MITOCHONDRIAL PRECURSOR (EC 1.14.-.-) (P450- CC24) (VITAMIN D(3) 24-HYDROXYLASE) (1,25-DIHYDROXYVITAMIN D(3) 24-HYDROXYLASE) (24-OHASE) - HOMO SAPIENS (HUMAN), 513 aa	1.90E-279	20
1271	cg43143315	3396	TGTGAAATTATTTTAGAATTATAA[A/gap]TTCACGTCTTGTCAGATTTCATCTG	A	gap		SILENT-NONCODING	cyto450	Human Gene SWISSNEW-ID:Q07973 CYTOCHROME P450-CC24 MITOCHONDRIAL PRECURSOR (EC 1.14.-.-) (P450- CC24) (VITAMIN D(3) 24-HYDROXYLASE) (1,25-DIHYDROXYVITAMIN D(3) 24-HYDROXYLASE) (24-OHASE) - HOMO SAPIENS (HUMAN), 513 aa.	pcis:SWISSPROT-ID:Q07973 CYTOCHROME P450-CC24 MITOCHONDRIAL PRECURSOR (EC 1.14.-.-) (P450- CC24) (VITAMIN D(3) 24-HYDROXYLASE) (1,25-DIHYDROXYVITAMIN D(3) 24-HYDROXYLASE) (24-OHASE) - HOMO SAPIENS (HUMAN), 513 aa	1.90E-279	20

1272	cg43143315	3411	AGAATTATAAATT CACGTCTTGTCA[G/T]ATTTCATCTG TATACCTTCAAAT TC	G	T			SILENT-NONCODING	cyto450	Human Gene SWISSNEW-ID:Q07973 CYTOCHROME P450-CC24 MITOCHONDRIAL PRECURSOR (EC 1.14.-.-) (P450- CC24) (VITAMIN D(3) 24-HYDROXYLASE) (1,25-DIHYDROXYVITAMIN D(3) 24-HYDROXYLASE) (24-OHASE) - HOMO SAPIENS (HUMAN), 513 aa.lpcls:SWISSPROT-ID:Q07973 CYTOCHROME P450-CC24 MITOCHONDRIAL PRECURSOR (EC 1.14.-.-) (P450- CC24) (VITAMIN D(3) 24-HYDROXYLASE) (1,25-DIHYDROXYVITAMIN D(3) 24-HYDROXYLASE) (24-OHASE) - HOMO SAPIENS (HUMAN), 513 aa.	1.90E-279	20
1273	cg34413296	1732	CGCTGTGAACAT GTCCAGGCGCG GC[T/gap]GCTTC TCCATCAATTGA AGAAGACA	T	gap			SILENT-NONCODING	cyto450	Human Gene SWISSNEW-ID:P05177 CYTOCHROME P450 1A2 (EC 1.14.14.1) (CYPIA2) (P450-P3) (P(3)450) (P450 4) - HOMO SAPIENS (HUMAN), 515 aa.lpcls:SWISSPROT-ID:P05177 CYTOCHROME P450 IA2 (EC 1.14.14.1) (P450-P3) (P450-4) - HOMO SAPIENS (HUMAN), 515 aa.	4.60E-278	15 (15q22)
1274	cg43309495	230	TTCTCTCCCTCC TCATCTGAGACA T[G/gap]GCAGCA GCCAGGAACCA CTGTGCCA	G	gap			SILENT-NONCODING	cytochrome	Human Gene SPTREMBL-ID:Q64639 CYTOCHROME P-450C27/25 (EC 1.14.14.1) - RATTUS NORVEGICUS (RAT), 540 aa.	1.90E-202	2 (2q33)
1275	cg43923430	130	AGAACTGTATAG GAAGCATGGCG CT[gap/G]GGCAT CTGCTTCTGGTG AGGGCCTC	gap	G			SILENT-NONCODING	cytochrome	Human Gene Similar to SWISSPROT-ID:P40086 CYTOCHROME C OXIDASE ASSEMBLY PROTEIN COX15 - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 486 aa.	3.70E-54	10

1276	cg43923430	132	GAACTGTATAGGAAGCATGGCGCTG[G/gap]CATCTGCTTCTGGTGAGGGCCTCAC	G	gap			SILENT-NONCODING	cytochrome	Human Gene Similar to SWISSPROT-ID:P40086 CYTOCHROME C OXIDASE ASSEMBLY PROTEIN COX15 - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 486 aa.	3.70E-54	10
1277	cg43923430	2721	CTGATGCAATCACACTGTGCTCTAG[G/gap]CGCTGCCCTAGGAGCCAGGAGCGGC	G	gap			SILENT-NONCODING	cytochrome	Human Gene Similar to SWISSPROT-ID:P40086 CYTOCHROME C OXIDASE ASSEMBLY PROTEIN COX15 - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 486 aa.	3.70E-54	10
1278	cg43923430	2744	AGGCGCTGCCCTAGGAGCCAGGAGC[G/gap]GCAGATACTGCCTCCCCTTCAAGGC	G	gap			SILENT-NONCODING	cytochrome	Human Gene Similar to SWISSPROT-ID:P40086 CYTOCHROME C OXIDASE ASSEMBLY PROTEIN COX15 - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 486 aa.	3.70E-54	10
1279	cg43923430	390	CCCACCTCTAACACTGAATGTCACA[C/gap]TTTGAACATGAGATTTGGAGGGGAC	C	gap			SILENT-NONCODING	cytochrome	Human Gene Similar to SWISSPROT-ID:P40086 CYTOCHROME C OXIDASE ASSEMBLY PROTEIN COX15 - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 486 aa.	3.70E-54	10
1280	cg43923204	1029	AAAATGCAGGCCCTGGCTCAGTCAC[C/A]AGGAAGGGGGTGCTCCGAGGCCTTT	C	A			SILENT-NONCODING	cytochrome	Human Gene Similar to SWISSPROT-ID:P21592 CYTOCHROME C OXIDASE ASSEMBLY PROTEIN COX10 PRECURSOR - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 462 aa.	1.70E-52	17
1281	cg43923204	114	TGTGAAGGCTGTAACAAGTTGTAGA[G/A]GCTTTTTCCAGACATTCCTATGCAA	G	A			SILENT-NONCODING	cytochrome	Human Gene Similar to SWISSPROT-ID:P21592 CYTOCHROME C OXIDASE ASSEMBLY PROTEIN COX10 PRECURSOR - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 462 aa.	1.70E-52	17

1282	cg43923204	1258	TGGGGTTGGAG GAGAGATGTATA AA[gap/A]GACCC TCAAAGGGAAAA ATAATTCC	gap	A			SILENT-NONCODING	cytochrome	Human Gene Similar to SWISSPROT-ID:P21592 CYTOCHROME C OXIDASE ASSEMBLY PROTEIN COX10 PRECURSOR - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 462 aa.	1.70E-52	17
1283	cg43923204	277	CTGTTTAAATGTT GTTTAACTCTCC[C/T]ACCCCGACC AATGAATCCCTA CGGA	C	T			SILENT-NONCODING	cytochrome	Human Gene Similar to SWISSPROT-ID:P21592 CYTOCHROME C OXIDASE ASSEMBLY PROTEIN COX10 PRECURSOR - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 462 aa.	1.70E-52	17
1284	cg43923204	289	GTTTAACTCTCC CACCCCGACCAA T[gap/C]GAATCC CTACGGACCAGC AGTGCCC	gap	C			SILENT-NONCODING	cytochrome	Human Gene Similar to SWISSPROT-ID:P21592 CYTOCHROME C OXIDASE ASSEMBLY PROTEIN COX10 PRECURSOR - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 462 aa.	1.70E-52	17
1285	cg43923204	296	CTCTCCCACCCC GACCAATGAATC C[C/gap]TACGGA CCAGCAGTGCC CTGGGAGA	C	gap			SILENT-NONCODING	cytochrome	Human Gene Similar to SWISSPROT-ID:P21592 CYTOCHROME C OXIDASE ASSEMBLY PROTEIN COX10 PRECURSOR - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 462 aa.	1.70E-52	17
1286	cg43923204	307	CGACCAATGAAT CCCTACGGACCA G[C/T]AGTGCCCT GGGAGACTGAG TAATGA	C	T			SILENT-NONCODING	cytochrome	Human Gene Similar to SWISSPROT-ID:P21592 CYTOCHROME C OXIDASE ASSEMBLY PROTEIN COX10 PRECURSOR - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 462 aa.	1.70E-52	17
1287	cg43923204	330	GCAGTGCCCTG GGAGACTGAGTA AT[gap/C]GAAAA CATCCTGTCAAG CTTCAAGA	gap	C			SILENT-NONCODING	cytochrome	Human Gene Similar to SWISSPROT-ID:P21592 CYTOCHROME C OXIDASE ASSEMBLY PROTEIN COX10 PRECURSOR - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 462 aa.	1.70E-52	17

1288	cg43923204	378	AGACCTTTGGGC AGATGGGACTCT G[C/T]AGACCCG TGGGAGCACAAA GGACTA	C	T			SILENT-NONCODING	cytochrome	Human Gene Similar to SWISSPROT-ID:P21592 CYTOCHROME C OXIDASE ASSEMBLY PROTEIN COX10 PRECURSOR - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 462 aa.	1.70E-52	17
1289	cg43923204	421	AAGGACTAAAAA GCTGCAGGTAAC C[G/A]TATTTGGT AACCGAGACCAC ACCTG	G	A			SILENT-NONCODING	cytochrome	Human Gene Similar to SWISSPROT-ID:P21592 CYTOCHROME C OXIDASE ASSEMBLY PROTEIN COX10 PRECURSOR - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 462 aa.	1.70E-52	17
1290	cg43923204	423	GGACTAAAAAGC TGCAGGTAACCG T[A/G]TTTGGTAA CCGAGACCACAC CTGGC	A	G			SILENT-NONCODING	cytochrome	Human Gene Similar to SWISSPROT-ID:P21592 CYTOCHROME C OXIDASE ASSEMBLY PROTEIN COX10 PRECURSOR - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 462 aa.	1.70E-52	17
1291	cg43275625	92	TTTCTTTTTATTG AGAACATCTCAA[A/G]TCCTTTGTC TGTATTTGACAG CGTC	A	G			SILENT-NONCODING	deaminase	Human Gene SPTREMBL-ID:O00465 DSRNA ADENOSINE DEAMINASE DRADA2C - HOMO SAPIENS (HUMAN), 714 aa.	0	21
1292	cg43318865	1205	GAGACCCCTGG AGGGGCTGGAG TTT[T/gap]ATCCA GCGCCTCGTCGT ATGTTTGG	T	gap			SILENT-NONCODING	deaminase	Human Gene SWISSPROT-ID:P20132 L-SERINE DEHYDRATASE (EC 4.2.1.13) (L-SERINE DEAMINASE) - HOMO SAPIENS (HUMAN), 328 aa.	1.1E-173	12
1293	cg43318865	1246	TATGTTTGGCTG AGCACCTGTGGC C[gap/C]TGGGTG CAGGTTAACTTC TTGTTAT	gap	C			SILENT-NONCODING	deaminase	Human Gene SWISSPROT-ID:P20132 L-SERINE DEHYDRATASE (EC 4.2.1.13) (L-SERINE DEAMINASE) - HOMO SAPIENS (HUMAN), 328 aa.	1.1E-173	12

1294	cg41626024	838	TGGGACTTAGAA CACCGCCGCCC CC[C/gap]TGCCC CACCTTTCCTTT CCTTCCTG	C	gap			SILENT-NONCODING	deaminase	Human Gene Similar to SWISSPROT-ID:P32320 CYTIDINE DEAMINASE (EC 3.5.4.5) (CYTIDINE AMINOHYDROLASE) - HOMO SAPIENS (HUMAN), 146 aa.\|pdb:TREMBLNEW-ID:E1228801 CYTIDINE DEAMINASE (EC 3.5.4.5) - HOMO SAPIENS (HUMAN), 146 aa.	8.8E-78	1 (1p36.2)
1295	cg43967318	133	GGCACAGTGCT GGGAACACTAG GCC[C/gap]CTTC GGGACAAACCA GGGCCTTAAG	C	gap			SILENT-NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P49748 ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC PRECURSOR (EC 1.3.99.-) (VLCAD) - HOMO SAPIENS (HUMAN), 655 aa.	0	17 (17p11.2)
1296	cg43967318	134	GCACAGTGCTG GGAACACTAGGC CC[C/gap]TTCGG GACAAACCAGG GCCTTAAGG	C	gap			SILENT-NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P49748 ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC PRECURSOR (EC 1.3.99.-) (VLCAD) - HOMO SAPIENS (HUMAN), 655 aa.	0	17 (17p11.2)
1297	cg43967318	210	GGAAGGCACATA ACTGGGACAGG CC[C/gap]TGGCG GGGAGTATTCAG AAGCCAAG	C	gap			SILENT-NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P49748 ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC PRECURSOR (EC 1.3.99.-) (VLCAD) - HOMO SAPIENS (HUMAN), 655 aa.	0	17 (17p11.2)
1298	cg43967318	215	GCACATAACTGG GACAGGCCCTG GC[G/C]GGGAGT ATTCAGAAGCCA AGTGGGT	G	C			SILENT-NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P49748 ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC PRECURSOR (EC 1.3.99.-) (VLCAD) - HOMO SAPIENS (HUMAN), 655 aa.	0	17 (17p11.2)
1299	cg44033747	3686	ATCTGTAATCAC ATTTCTGAGTGT T[T/C]TCCTCTTT TTCTGTGTGAGG TTTTT	T	C			SILENT-NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P23378 GLYCINE DEHYDROGENASE (DECARBOXYLATING) PRECURSOR (EC 1.4.4.2) (GLYCINE DECARBOXYLASE) (GLYCINE CLEAVAGE SYSTEM P-PROTEIN) - HOMO SAPIENS (HUMAN), 1020 aa.	0	9 (9p22)

1300	cg44033747	3707	TGTTTTCCTCTTTTTCTGTGTGAGG[T/gap]TTTTTTTTTTTTTAATCTGCATTTA	T	gap			SILENT-NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P23378 GLYCINE DEHYDROGENASE (DECARBOXYLATING) PRECURSOR (EC 1.4.4.2) (GLYCINE DECARBOXYLASE) (GLYCINE CLEAVAGE SYSTEM P-PROTEIN) - HOMO SAPIENS (HUMAN), 1020 aa.	0	9 (9p22)
1301	cg44033747	3720	TTCTGTGTGAGGTTTTTTTTTTTTT[T/gap]AATCTGCATTTATTAGTATTCTAAT	T	gap			SILENT-NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P23378 GLYCINE DEHYDROGENASE (DECARBOXYLATING) PRECURSOR (EC 1.4.4.2) (GLYCINE DECARBOXYLASE) (GLYCINE CLEAVAGE SYSTEM P-PROTEIN) - HOMO SAPIENS (HUMAN), 1020 aa.	0	9 (9p22)
1302	cg43314766	267	GCTAAATGCAACTGTTCCTTTTCTA[T/gap]AAAATTATTATCCTGCAAAAGTAGC	T	gap			SILENT-NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P00352 ALDEHYDE DEHYDROGENASE, CYTOSOLIC (EC 1.2.1.3) (CLASS 1) (ALHDII) (ALDH-E1) - HOMO SAPIENS (HUMAN), 500 aa.	7.2E-273	9 (9q21)
1303	cg43918671	1029	ACAATAAGTAGCTTTTTGTCTTACA[T/C]ATTAGTGCACTGAAACAAAATACTA	T	C			SILENT-NONCODING	dehydrogenase	Human Gene SPTREMBL-ID:Q14131 DIHYDROLIPOAMIDE DEHYDROGENASE - HOMO SAPIENS (HUMAN), 511 aa.	5.1E-272	7 (7q31)
1304	cg43918671	1218	GCTCCCAGGAAATTTCAGAAAAAAA[T/gap]ATATATAATCTTCTAATTCAAAAGT	T	gap			SILENT-NONCODING	dehydrogenase	Human Gene SPTREMBL-ID:Q14131 DIHYDROLIPOAMIDE DEHYDROGENASE - HOMO SAPIENS (HUMAN), 511 aa.	5.1E-272	7 (7q31)
1305	cg43918671	749	GGTTAAATAAAACAAGTGAGAGACC[A/G]TTTACTTACATCAGTTCGGTTTATA	A	G			SILENT-NONCODING	dehydrogenase	Human Gene SPTREMBL-ID:Q14131 DIHYDROLIPOAMIDE DEHYDROGENASE - HOMO SAPIENS (HUMAN), 511 aa.	5.1E-272	7 (7q31)
1306	cg43996714	391	TCATTCATGCTTCTTTTATCCTCTT[T/G]CTTTAGAAGTTCACAGTGTTATATA	T	G			SILENT-NONCODING	dehydrogenase	Human Gene TREMBLNEW-ID:G2979625 PYRUVATE DEHYDROGENASE COMPLEX PROTEIN X SUBUNIT PRECURSOR - HOMO SAPIENS (HUMAN), 501 aa.	1.6E-266	11

1307	cg43996714	549	TATTATCCAGAA TAAACTTCTGTA C[C/A]TATTAAAT TCTTCAAGTATAT CTAG	C	A			SILENT-NONCODING	dehydrogenase	Human Gene TREMBLNEW-ID:G2979625 PYRUVATE DEHYDROGENASE COMPLEX PROTEIN X SUBUNIT PRECURSOR - HOMO SAPIENS (HUMAN), 501 aa.	1.6E-266	11
1308	cg43330439	86	GCTGACCCTGTG TGAGGGCAAAG GG[T/C]TTTTTTT TGCAGGAACAGT GGTTTA	T	C			SILENT-NONCODING	dehydrogenase	Human Gene TREMBLNEW-ID:G2677802 PROLINE DEHYDROGENASE/PROLINE OXIDASE - HOMO SAPIENS (HUMAN), 516 aa.	2.1E-257	
1309	cg43330439	88	TGACCCTGTGTG AGGGCAAAGGG TT[T/C]TTTTTTG CAGGAACAGTG GTTTATT	T	C			SILENT-NONCODING	dehydrogenase	Human Gene TREMBLNEW-ID:G2677802 PROLINE DEHYDROGENASE/PROLINE OXIDASE - HOMO SAPIENS (HUMAN), 516 aa.	2.1E-257	
1310	cg43330439	92	CCTGTGTGAGG GCAAAGGGTTTT TT[T/G]TTGCAGG AACAGTGGTTTA TTGACC	T	G			SILENT-NONCODING	dehydrogenase	Human Gene TREMBLNEW-ID:G2677802 PROLINE DEHYDROGENASE/PROLINE OXIDASE - HOMO SAPIENS (HUMAN), 516 aa.	2.1E-257	
1311	cg43330439	93	CTGTGTGAGGG CAAAGGGTTTTT TT[T/C]TGCAGGA ACAGTGGTTTAT TGACCA	T	C			SILENT-NONCODING	dehydrogenase	Human Gene TREMBLNEW-ID:G2677802 PROLINE DEHYDROGENASE/PROLINE OXIDASE - HOMO SAPIENS (HUMAN), 516 aa.	2.1E-257	
1312	cg43264442	3020	TACTTGTGCTCT GCTGAGAATGTA C[A/G]GTTTGCAT TAAACATCCCAG GTCTC	A	G			SILENT-NONCODING	dehydrogenase	Human Gene TREMBLNEW-ID:G806944 UDP-GLUCOSE DEHYDROGENASE, UDPGDH=52 KDA SUBUNIT {EC 1.1.1.22} - BOS TAURUS, 468 aa.	8.6E-240	4
1313	cg43259523	1624	TCTGTCTTACTC TGTCACCCAGGC T[A/G]GAGTGCA GTGGCGCGATCT CAGCTC	A	G			SILENT-NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P45954 ACYL-COA DEHYDROGENASE, SHORT/BRANCHED CHAIN SPECIFIC PRECURSOR (EC 1.3.99.-) (SBCAD) (2-METHYL BRANCHED CHAIN ACYL-COA DEHYDROGENASE) (2-MEBCAD) - HOMO SAPIENS (HUMAN), 432 aa.	2E-229	10 (10q25)

1314	cg43259523	1625	CTGTCTTACTCT GTCACCCAGGCT A[G/A]AGTGCAGT GGCGCGATCTCA GCTCA	G	A			SILENT-NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P45954 ACYL-COA DEHYDROGENASE, SHORT/BRANCHED CHAIN SPECIFIC PRECURSOR (EC 1.3.99.-) (SBCAD) (2-METHYL BRANCHED CHAIN ACYL-COA DEHYDROGENASE) (2-MEBCAD) - HOMO SAPIENS (HUMAN), 432 aa.	2E-229	10 (10q25)
1315	cg43259523	1626	TGTCTTACTCTG TCACCCAGGCTA G[A/G]GTGCAGT GGCGCGATCTCA GCTCAC	A	G			SILENT-NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P45954 ACYL-COA DEHYDROGENASE, SHORT/BRANCHED CHAIN SPECIFIC PRECURSOR (EC 1.3.99.-) (SBCAD) (2-METHYL BRANCHED CHAIN ACYL-COA DEHYDROGENASE) (2-MEBCAD) - HOMO SAPIENS (HUMAN), 432 aa.	2E-229	10 (10q25)
1316	cg43259523	1642	CCAGGCTAGAGT GCAGTGGCGCG AT[C/T]TCAGCTC ACTGCAGCCTTG ACCTCC	C	T			SILENT-NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P45954 ACYL-COA DEHYDROGENASE, SHORT/BRANCHED CHAIN SPECIFIC PRECURSOR (EC 1.3.99.-) (SBCAD) (2-METHYL BRANCHED CHAIN ACYL-COA DEHYDROGENASE) (2-MEBCAD) - HOMO SAPIENS (HUMAN), 432 aa.	2E-229	10 (10q25)
1317	cg43259523	1643	CAGGCTAGAGTG CAGTGGCGCGA T[C/T]CAGCTCA CTGCAGCCTTGA CCTCCT	T	C			SILENT-NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P45954 ACYL-COA DEHYDROGENASE, SHORT/BRANCHED CHAIN SPECIFIC PRECURSOR (EC 1.3.99.-) (SBCAD) (2-METHYL BRANCHED CHAIN ACYL-COA DEHYDROGENASE) (2-MEBCAD) - HOMO SAPIENS (HUMAN), 432 aa.	2E-229	10 (10q25)

1318	cg43259523	1859	GCTGGGATTACAGGGATGAGCCACC[A/G]TGCCTGGCTGGGTATTTATATTATC	A	G			SILENT-NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P45954 ACYL-COA DEHYDROGENASE, SHORT/BRANCHED CHAIN SPECIFIC PRECURSOR (EC 1.3.99.-) (SBCAD) (2-METHYL BRANCHED CHAIN ACYL-COA DEHYDROGENASE) (2-MEBCAD) - HOMO SAPIENS (HUMAN), 432 aa.	2E-229	10 (10q25)
1319	cg43259523	2043	GTTACATAGTAGGCAATTTTTATCC[A/gap]GTACTTTATAGATTCAACTCTAAGT	A	gap			SILENT-NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P45954 ACYL-COA DEHYDROGENASE, SHORT/BRANCHED CHAIN SPECIFIC PRECURSOR (EC 1.3.99.-) (SBCAD) (2-METHYL BRANCHED CHAIN ACYL-COA DEHYDROGENASE) (2-MEBCAD) - HOMO SAPIENS (HUMAN), 432 aa.	2E-229	10 (10q25)
1320	cg43259523	2365	AAATATTCAATACAGTGTTGGATAT[T/gap]CTGTCATGCACTATTTTTCAGTTGA	T	gap			SILENT-NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P45954 ACYL-COA DEHYDROGENASE, SHORT/BRANCHED CHAIN SPECIFIC PRECURSOR (EC 1.3.99.-) (SBCAD) (2-METHYL BRANCHED CHAIN ACYL-COA DEHYDROGENASE) (2-MEBCAD) - HOMO SAPIENS (HUMAN), 432 aa.	2E-229	10 (10q25)
1321	cg43259523	2383	TGGATATTCTGTCATGCACTATTTT[T/gap]CAGTTGACAATTTCTGTATTTTAAT	T	gap			SILENT-NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P45954 ACYL-COA DEHYDROGENASE, SHORT/BRANCHED CHAIN SPECIFIC PRECURSOR (EC 1.3.99.-) (SBCAD) (2-METHYL BRANCHED CHAIN ACYL-COA DEHYDROGENASE) (2-MEBCAD) - HOMO SAPIENS (HUMAN), 432 aa.	2E-229	10 (10q25)

1322	cg43259523	2437	TACTGTTTCTTCA GTCATGGTTATT[gap/A]GCACTTTA TCCTGAATAATA ATTCA	gap	A			SILENT-NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P45954 ACYL-COA DEHYDROGENASE, SHORT/BRANCHED CHAIN SPECIFIC PRECURSOR (EC 1.3.99.-) (SBCAD) (2-METHYL BRANCHED CHAIN ACYL-COA DEHYDROGENASE) (2-MEBCAD) - HOMO SAPIENS (HUMAN), 432 aa.	2E-229	10 (10q25)
1323	cg43259523	2458	TTATTGCACTTTA TCCTGAATAATA[A/G]TTCAGAAAT TGGGTTTTGGTT CAGT	A	G			SILENT-NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P45954 ACYL-COA DEHYDROGENASE, SHORT/BRANCHED CHAIN SPECIFIC PRECURSOR (EC 1.3.99.-) (SBCAD) (2-METHYL BRANCHED CHAIN ACYL-COA DEHYDROGENASE) (2-MEBCAD) - HOMO SAPIENS (HUMAN), 432 aa.	2E-229	10 (10q25)
1324	cg43259523	2564	GAATGAGGGAG AGAAGGGGGCT GTA[G/C]AGTTTG AAAAAGCATATT CAATATT	G	C			SILENT-NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P45954 ACYL-COA DEHYDROGENASE, SHORT/BRANCHED CHAIN SPECIFIC PRECURSOR (EC 1.3.99.-) (SBCAD) (2-METHYL BRANCHED CHAIN ACYL-COA DEHYDROGENASE) (2-MEBCAD) - HOMO SAPIENS (HUMAN), 432 aa.	2E-229	10 (10q25)
1325	cg43259523	2650	CTATTGTTTTGC AATATAGGTTAT A[A/gap]ACAGGC AAAATGCAATAA AATATAT	A	gap			SILENT-NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P45954 ACYL-COA DEHYDROGENASE, SHORT/BRANCHED CHAIN SPECIFIC PRECURSOR (EC 1.3.99.-) (SBCAD) (2-METHYL BRANCHED CHAIN ACYL-COA DEHYDROGENASE) (2-MEBCAD) - HOMO SAPIENS (HUMAN), 432 aa.	2E-229	10 (10q25)

1326	cg43259523	2651	TATTGTTTTGCAA TATAGGTTATAA[A/gap]CAGGCAAA ATGCAATAAAAT ATATA	A	gap			SILENT-NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P45954 ACYL-COA DEHYDROGENASE, SHORT/BRANCHED CHAIN SPECIFIC PRECURSOR (EC 1.3.99.-) (SBCAD) (2-METHYL BRANCHED CHAIN ACYL-COA DEHYDROGENASE) (2-MEBCAD) - HOMO SAPIENS (HUMAN), 432 aa.	2E-229	10 (10q25)
1327	cg43259523	2656	TTTTGCAATATA GGTTATAAACAG G[C/gap]AAAATG CAATAAAATATAT ATCTGG	C	gap			SILENT-NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P45954 ACYL-COA DEHYDROGENASE, SHORT/BRANCHED CHAIN SPECIFIC PRECURSOR (EC 1.3.99.-) (SBCAD) (2-METHYL BRANCHED CHAIN ACYL-COA DEHYDROGENASE) (2-MEBCAD) - HOMO SAPIENS (HUMAN), 432 aa.	2E-229	10 (10q25)
1328	cg43057018	1713	ATTTGATGAACC AAGGAAAGCCAT G[C/A]GTTTAAAC AAATATTTACATT TAAT	C	A			SILENT-NONCODING	dehydrogenase	Human Gene SWISSNEW-ID:P08319 ALCOHOL DEHYDROGENASE CLASS II PI CHAIN (EC 1.1.1.1) - HOMO SAPIENS (HUMAN), 391 aa.\|pcls:SWISSPROT-ID:P08319 ALCOHOL DEHYDROGENASE CLASS II PI CHAIN (EC 1.1.1.1) - HOMO SAPIENS (HUMAN), 391 aa.	1.3E-209	4 (4q22)
1329	cg43057018	1805	CTGTTATATATAT GAATATTCCCTA[T/C]GTTAAATAAT AATAATAACTAG TGT	T	C			SILENT-NONCODING	dehydrogenase	Human Gene SWISSNEW-ID:P08319 ALCOHOL DEHYDROGENASE CLASS II PI CHAIN (EC 1.1.1.1) - HOMO SAPIENS (HUMAN), 391 aa.\|pcls:SWISSPROT-ID:P08319 ALCOHOL DEHYDROGENASE CLASS II PI CHAIN (EC 1.1.1.1) - HOMO SAPIENS (HUMAN), 391 aa.	1.3E-209	4 (4q22)
1330	cg44016790	1302	CCATCTTGAGCC ATGTCCCCCAGC C[A/gap]TGGCAT GGGTGCACTGTA AACGCCA	A	gap			SILENT-NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:Q02127 DIHYDROOROTATE DEHYDROGENASE PRECURSOR (EC 1.3.3.1) (DIHYDROOROTATE OXIDASE) - HOMO SAPIENS (HUMAN), 396 aa (fragment).	1.4E-207	16

1331	cg44016790	1310	AGCCATGTCCCCCAGCCATGGCATG[G/C]GTGCACTGTAAACGCCAATCGGGGG	G	C			SILENT-NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:Q02127 DIHYDROOROTATE DEHYDROGENASE PRECURSOR (EC 1.3.3.1) (DIHYDROOROTATE OXIDASE) - HOMO SAPIENS (HUMAN), 396 aa (fragment).	1.4E-207	16
1332	cg44016790	1311	GCCATGTCCCCCAGCCATGGCATGG[G/C]TGCACTGTAAACGCCAATCGGGGGG	G	C			SILENT-NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:Q02127 DIHYDROOROTATE DEHYDROGENASE PRECURSOR (EC 1.3.3.1) (DIHYDROOROTATE OXIDASE) - HOMO SAPIENS (HUMAN), 396 aa (fragment).	1.4E-207	16
1333	cg3000385	494	AACAGAGTGAACTGAGCATCAGTCA[G/C]AAAAAGTCTATGTTTGCAGAAATAC	G	C			SILENT-NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P40394 ALCOHOL DEHYDROGENASE CLASS IV MU/SIGMA CHAIN (EC 1.1.1.1) (RETINOL DEHYDROGENASE) (GASTRIC ALCOHOL DEHYDROGENASE) - HOMO SAPIENS (HUMAN), 374 aa.	4.4E-202	4 (4q23)
1334	cg3000385	530	TGTTTGCAGAAATACAGATCCAAGA[C/G]AAAGACAGGATGGGCACTGCTGGAA	C	G			SILENT-NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P40394 ALCOHOL DEHYDROGENASE CLASS IV MU/SIGMA CHAIN (EC 1.1.1.1) (RETINOL DEHYDROGENASE) (GASTRIC ALCOHOL DEHYDROGENASE) - HOMO SAPIENS (HUMAN), 374 aa.	4.4E-202	4 (4q23)
1335	cg43923979	126	TATCTTGTTTGGATACATCTTTCAT[C/G]AGGACTCTGCCACATCCATACTTTG	C	G			SILENT-NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P11177 PYRUVATE DEHYDROGENASE E1 COMPONENT, BETA SUBUNIT PRECURSOR (EC 1.2.4.1) (PDHE1-B) - HOMO SAPIENS (HUMAN), 359 aa.	4E-192	3 (3p13)
1336	cg43923979	179	CTTGTGGTGAGAGAGGATAAAATGT[T/G]ATATAATTTGTTATTCAAAGAACAT	T	G			SILENT-NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P11177 PYRUVATE DEHYDROGENASE E1 COMPONENT, BETA SUBUNIT PRECURSOR (EC 1.2.4.1) (PDHE1-B) - HOMO SAPIENS (HUMAN), 359 aa.	4E-192	3 (3p13)

1337	cg43923979	323	AATACCTGCTGT TGCTTTAGAAAT C[G/A]TTTTCCGT TATGAATAGTCA GGTCT	G	A			SILENT-NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P11177 PYRUVATE DEHYDROGENASE E1 COMPONENT, BETA SUBUNIT PRECURSOR (EC 1.2.4.1) (PDHE1-B) - HOMO SAPIENS (HUMAN), 359 aa.	4E-192	3 (3p13)
1338	cg43923979	330	GCTGTTGCTTTA GAAATCGTTTTC C[G/T]TTATGAAT AGTCAGGTCTTG CAGTA	G	T			SILENT-NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P11177 PYRUVATE DEHYDROGENASE E1 COMPONENT, BETA SUBUNIT PRECURSOR (EC 1.2.4.1) (PDHE1-B) - HOMO SAPIENS (HUMAN), 359 aa.	4E-192	3 (3p13)
1339	cg43923979	69	ATCAAAACAAC TAACAGTAAATG T[A/G]TATTATAT GCTTTAATTTTAT ACAT	A	G			SILENT-NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P11177 PYRUVATE DEHYDROGENASE E1 COMPONENT, BETA SUBUNIT PRECURSOR (EC 1.2.4.1) (PDHE1-B) - HOMO SAPIENS (HUMAN), 359 aa.	4E-192	3 (3p13)
1340	cg43998926	248	TGACCCAGACAG GGATATCATTGC T[A/gap]AAAAAA AAAAATCCCCTT GTGACC	A	gap			SILENT-NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P50213 ISOCITRATE DEHYDROGENASE (NAD), MITOCHONDRIAL SUBUNIT ALPHA PRECURSOR (EC 1.1.1.41) (ISOCITRIC DEHYDROGENASE) (NAD+ SPECIFIC ICDH) - HOMO SAPIENS (HUMAN), 366 aa.	1.3E-190	15
1341	cg43998926	260	GGATATCATTGC TAAAAAAAAAA A[A/gap]TCCCCT TGTGACCTGGGT ACATTTT	A	gap			SILENT-NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P50213 ISOCITRATE DEHYDROGENASE (NAD), MITOCHONDRIAL SUBUNIT ALPHA PRECURSOR (EC 1.1.1.41) (ISOCITRIC DEHYDROGENASE) (NAD+ SPECIFIC ICDH) - HOMO SAPIENS (HUMAN), 366 aa.	1.3E-190	15
1342	cg43998926	260	GATATCATTGCT AAAAAAAAAAA A[gap/A]TCCCCT TGTGACCTGGGT ACATTTT	gap	A			SILENT-NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P50213 ISOCITRATE DEHYDROGENASE (NAD), MITOCHONDRIAL SUBUNIT ALPHA PRECURSOR (EC 1.1.1.41) (ISOCITRIC DEHYDROGENASE) (NAD+ SPECIFIC ICDH) - HOMO SAPIENS (HUMAN), 366 aa.	1.3E-190	15

1343	cg43998926	339	AAGGGCCAAAG GAGGCCATGAGT TG[T/gap]CTTTG GTTGTGGGGACA GAGGGTAA	T	gap			SILENT-NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P50213 ISOCITRATE DEHYDROGENASE (NAD), MITOCHONDRIAL SUBUNIT ALPHA PRECURSOR (EC 1.1.1.41) (ISOCITRIC DEHYDROGENASE) (NAD+ SPECIFIC ICDH) - HOMO SAPIENS (HUMAN), 366 aa.	1.30E-190	15
1344	cg43998926	445	GAGAAGGGAGA GGAAGACAGGA AGG[G/A]AAAGG AGATGCCTGAGG GTCAAAAG	G	A			SILENT-NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P50213 ISOCITRATE DEHYDROGENASE (NAD), MITOCHONDRIAL SUBUNIT ALPHA PRECURSOR (EC 1.1.1.41) (ISOCITRIC DEHYDROGENASE) (NAD+ SPECIFIC ICDH) - HOMO SAPIENS (HUMAN), 366 aa.	1.30E-190	15
1345	cg43948373	1817	AACATCCCTTAA TTTGAGGTGTTC C[A/T]GCAGCTGT TTTTGGAGAAGA CAAAG	A	T			SILENT-NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P46562 HYPOTHETICAL ALDEHYDE-DEHYDROGENASE LIKE PROTEIN F01F1.6 - CAENORHABDITIS ELEGANS, 514 aa.	2.80E-184	5
1346	cg43948373	1828	ATTTGAGGTGTT CCAGCAGCTGTT T[T/C]TGGAGAAG ACAAAGAAAATT AAAGT	T	C			SILENT-NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P46562 HYPOTHETICAL ALDEHYDE-DEHYDROGENASE LIKE PROTEIN F01F1.6 - CAENORHABDITIS ELEGANS, 514 aa.	2.80E-184	5
1347	cg43948373	1845	AGCTGTTTTTGG AGAAGACAAAGA A[A/G]ATTAAAGT TTTCCCTGAATA AATGC	A	G			SILENT-NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P46562 HYPOTHETICAL ALDEHYDE-DEHYDROGENASE LIKE PROTEIN F01F1.6 - CAENORHABDITIS ELEGANS, 514 aa.	2.80E-184	5
1348	cg43948373	1873	TAAAGTTTTCCC TGAATAAATGCA T[T/C]ATTATGAC TGTGACAGTGAC TAATC	T	C			SILENT-NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P46562 HYPOTHETICAL ALDEHYDE-DEHYDROGENASE LIKE PROTEIN F01F1.6 - CAENORHABDITIS ELEGANS, 514 aa.	2.80E-184	5

1349	cg43255016	114	AATATCATCATTGGCTCTGAAATGC[G/A]TCTAAAGATGTCATTCTTAAGTCAA	G	A			SILENT-NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P29266 3-HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR (EC 1.1.1.31) (HIBADH) - RATTUS NORVEGICUS (RAT), 346 aa (fragment).	3.40E-156	
1350	cg43255016	159	AGTCAAAAAATACGTAGTAAGAATG[T/A]ACAAGAAAGAAAAAAATATAAAAC	T	A			SILENT-NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P29266 3-HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR (EC 1.1.1.31) (HIBADH) - RATTUS NORVEGICUS (RAT), 346 aa (fragment).	3.40E-156	
1351	cg43255016	168	ATACGTAGTAAGAATGTACAAGAAA[G/A]AAAAAAATATAAAAACAAGTCTGCT	G	A			SILENT-NONCODING	dehydrogenase	Human Gene SWISSPROT-ID:P29266 3-HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR (EC 1.1.1.31) (HIBADH) - RATTUS NORVEGICUS (RAT), 346 aa (fragment).	3.40E-156	
1352	cg43941594	1818	CCGAGGACCGCCCTTGGAGTGGCAC[C/T]TGTTGAGAGGATGGCCTGCATAGAT	C	T			SILENT-NONCODING	dehydrogenase	Human Gene Homologous to SWISSPROT-ID:P13707 GLYCEROL-3-PHOSPHATE DEHYDROGENASE (NAD+), CYTOPLASMIC (EC 1.1.1.8) (GPD-C) (GPDH-C) - MUS MUSCULUS (MOUSE), 348 aa.	1.90E-137	3
1353	cg43941594	2210	TGTCTTGTTACCTCTGAGCCTTGAC[G/A]AAGGCATATTCTGACAACTAACGAA	G	A			SILENT-NONCODING	dehydrogenase	Human Gene Homologous to SWISSPROT-ID:P13707 GLYCEROL-3-PHOSPHATE DEHYDROGENASE (NAD+), CYTOPLASMIC (EC 1.1.1.8) (GPD-C) (GPDH-C) - MUS MUSCULUS (MOUSE), 348 aa.	1.90E-137	3
1354	cg43941594	238	TGTGGATGCCATGGGGCCATGCTGT[A/gap]GTCAAAAGTTAAATGAAAAACCACA	A	gap			SILENT-NONCODING	dehydrogenase	Human Gene Homologous to SWISSPROT-ID:P13707 GLYCEROL-3-PHOSPHATE DEHYDROGENASE (NAD+), CYTOPLASMIC (EC 1.1.1.8) (GPD-C) (GPDH-C) - MUS MUSCULUS (MOUSE), 348 aa.	1.90E-137	3

1355	cg4394159 4	322	TCATTCAGATATT TTGTTCCATATTA[T/C]AGGAGGGTG GATCCTAGCAAG GCAA	T	C			SILENT-NONCODING	dehydrogenase	Human Gene Homologous to SWISSPROT-ID:P13707 GLYCEROL-3-PHOSPHATE DEHYDROGENASE (NAD+), CYTOPLASMIC (EC 1.1.1.8) (GPD-C) (GPDH-C) - MUS MUSCULUS (MOUSE), 348 aa.	1.90E-137	3
1356	cg4394159 4	754	GCTACTTACTAG ACACCACAATTA G[C/gap]TTACAG CCCTTTATATATC TTTTAA	C	gap			SILENT-NONCODING	dehydrogenase	Human Gene Homologous to SWISSPROT-ID:P13707 GLYCEROL-3-PHOSPHATE DEHYDROGENASE (NAD+), CYTOPLASMIC (EC 1.1.1.8) (GPD-C) (GPDH-C) - MUS MUSCULUS (MOUSE), 348 aa.	1.90E-137	3
1357	cg4399107 0	297	GGGGTCAGCAAT TCCATTCTCTCT C[T/gap]CCGGCT CAGTTCAGAAGC TGTGATG	T	gap			SILENT-NONCODING	dehydrogenase	Human Gene Similar to TREMBLNEW-ID:E321870 VERY-LONG-CHAIN ACYL-COA DEHYDROGENASE - MUS MUSCULUS (MOUSE), 656 aa.	4.70E-95	3
1358	cg4400021 9	353	AGCGCAGGCTCT GAGAGCCGGGA CG[C/A]GTACAG CTATGTGGTGGT GGGCGCG	C	A			SILENT-NONCODING	dehydrogenase	Human Gene Similar to SPTREMBL-ID:Q64644 CHOLINE DEHYDROGENASE (EC 1.1.99.1) - RATTUS NORVEGICUS (RAT), 441 aa (fragment).	3.30E-93	

1359	cg43104003	266	AAATGTTACCTTTC[C/T]TAGTTCACACTC[C/T]TAATCCCTTAGTCCCCATAAAATAA	C	T		SILENT-NONCODING	dehydrogenase	Human Gene Similar to SWISSNEW-ID:P11586 C-1-TETRAHYDROFOLATE SYNTHASE, CYTOPLASMIC (C1-THF SYNTHASE) (METHYLENETETRAHYDROFOLATE DEHYDROGENASE (EC 1.5.1.5) / METHENYLTETRAHYDROFOLATE CYCLOHYDROLASE (EC 3.5.4.9) / FORMYLTETRAHYDROFOLATE SYNTHETASE (EC 6.3.4.3)) - HOMO SAPIENS (HUMAN), 934 aa.\|pdb:SWISSPROT-ID:P11586 C-1-TETRAHYDROFOLATE SYNTHASE, CYTOPLASMIC (METHYLENETETRAHYDROFOLATE DEHYDROGENASE (EC 1.5.1.5) / METHENYLTETRAHYDROFOLATE CYCLOHYDROLASE (EC 3.5.4.9) / FORMYLTETRAHYDROFOLATE SYNTHETASE (EC 6.3.4.3)) (C1-THF SYNTHASE) - HOMO SAPIENS (HUMAN), 934 aa.	7.10E-92	6

1360	cg43104003	452	AAGAAATCTTTG GCCTATTTCACC A[T/C]GTCTCCAG CATTGCATAACA GACAT	T	C			SILENT-NONCODING	dehydrogenase	Human Gene Similar to SWISSNEW-ID:P11586 C-1-TETRAHYDROFOLATE SYNTHASE, CYTOPLASMIC (C1-THF SYNTHASE) (METHYLENETETRAHYDROFOLATE DEHYDROGENASE (EC 1.5.1.5) / METHENYLTETRAHYDROFOLATE CYCLOHYDROLASE (EC 3.5.4.9) / FORMYLTETRAHYDROFOLATE SYNTHETASE (EC 6.3.4.3)) - HOMO SAPIENS (HUMAN), 934 aa.	pcls:SWISSPROT-ID:P11586 C-1-TETRAHYDROFOLATE SYNTHASE, CYTOPLASMIC (METHYLENETETRAHYDROFOLATE DEHYDROGENASE (EC 1.5.1.5) / METHENYLTETRAHYDROFOLATE CYCLOHYDROLASE (EC 3.5.4.9) / FORMYLTETRAHYDROFOLATE SYNTHETASE (EC 6.3.4.3)) (C1-THF SYNTHASE) - HOMO SAPIENS (HUMAN), 934 aa.	7.10E-92	6

1361	cg43104003	547	AGTAGTCTGTTT CAGGAGTCTGCA T[C/A]GGGTCCT GTGAGAGCCTTG TCCACT	C	A		SILENT-NONCODING	dehydrogenase	Human Gene Similar to SWISSNEW-ID:P11586 C-1-TETRAHYDROFOLATE SYNTHASE, CYTOPLASMIC (C1-THF SYNTHASE) (METHYLENETETRAHYDROFOLATE DEHYDROGENASE (EC 1.5.1.5) / METHENYLTETRAHYDROFOLATE CYCLOHYDROLASE (EC 3.5.4.9) / FORMYLTETRAHYDROFOLATE SYNTHETASE (EC 6.3.4.3)) - HOMO SAPIENS (HUMAN), 934 aa.\|pcls:SWISSPROT-ID:P11586 C-1-TETRAHYDROFOLATE SYNTHASE, CYTOPLASMIC (METHYLENETETRAHYDROFOLATE DEHYDROGENASE (EC 1.5.1.5) / METHENYLTETRAHYDROFOLATE CYCLOHYDROLASE (EC 3.5.4.9) / FORMYLTETRAHYDROFOLATE SYNTHETASE (EC 6.3.4.3)) (C1-THF SYNTHASE) - HOMO SAPIENS (HUMAN), 934 aa.	7.10E-92	6
1362	cg43990226	103	ACACATGAGCTG TGGCTGCATTTC A[C/T]ACAGAAGC TGACACATCTCG CAGGA	C	T		SILENT-NONCODING	dehydrogenase	Human Gene Similar to SWISSPROT-ID:Q02218 2-OXOGLUTARATE DEHYDROGENASE E1 COMPONENT PRECURSOR (EC 1.2.4.2) (ALPHA-KETOGLUTARATE DEHYDROGENASE) - HOMO SAPIENS (HUMAN), 1002 aa.	1.70E-88	10
1363	cg43990226	388	AAGATGGGAGCA GCTGGGGGATG CT[C/gap]CAGCA CAGTAGCCTGCC TATAGGAC	C	gap		SILENT-NONCODING	dehydrogenase	Human Gene Similar to SWISSPROT-ID:Q02218 2-OXOGLUTARATE DEHYDROGENASE E1 COMPONENT PRECURSOR (EC 1.2.4.2) (ALPHA-KETOGLUTARATE DEHYDROGENASE) - HOMO SAPIENS (HUMAN), 1002 aa.	1.70E-88	10

1364	cg43990226	408	ATGCTCCAGCAC AGTAGCCTGCCT A[T/C]AGGACTCC TCTGGCTCCCTC AGTCC	T	C		SILENT-NONCODING	dehydrogenase	Human Gene Similar to SWISSPROT-ID:Q02218 2-OXOGLUTARATE DEHYDROGENASE E1 COMPONENT PRECURSOR (EC 1.2.4.2) (ALPHA-KETOGLUTARATE DEHYDROGENASE) - HOMO SAPIENS (HUMAN), 1002 aa.	1.70E-88	10
1365	cg43300900	479	CTTGGTCTGCGC TCCAGCGTGGG CC[T/C]GGCTGT GCAGGCACGAG GTGTCCAT	T	C		SILENT-NONCODING	dehydrogenase	Human Gene Similar to SWISSPROT-ID:P29918 NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 6 (EC 1.6.5.3) (NADH DEHYDROGENASE 1, CHAIN 6) (NDH-1, CHAIN 6) - PARACOCCUS DENITRIFICANS, 173 aa.	4.90E-61	
1366	cg44029571	1685	CCCAATGGAGAC TTTCTGATGCAT C[G/A]TTTTCTTT GCTGTGCCAAAG CAGGT	G	A		SILENT-NONCODING	dehydrogenase	Human Gene Similar to SWISSPROT-ID:Q02218 2-OXOGLUTARATE DEHYDROGENASE E1 COMPONENT PRECURSOR (EC 1.2.4.2) (ALPHA-KETOGLUTARATE DEHYDROGENASE) - HOMO SAPIENS (HUMAN), 1002 aa.	3.50E-53	7 (7p14)
1367	cg44029571	767	AGCCACCGGCA ACAAGAAGACCC AC[C/gap]TGACG GAGCTGCAGCG CCTCCTGGA	C	gap		SILENT-NONCODING	dehydrogenase	Human Gene Similar to SWISSPROT-ID:Q02218 2-OXOGLUTARATE DEHYDROGENASE E1 COMPONENT PRECURSOR (EC 1.2.4.2) (ALPHA-KETOGLUTARATE DEHYDROGENASE) - HOMO SAPIENS (HUMAN), 1002 aa.	3.50E-53	7 (7p14)
1368	cg43918191	1244	CTGCCATGACTC ACAGGCAAAGGA G[G/gap]CAGGTC TGCCACCTGCGC TGCCGCT	G	gap		SILENT-NONCODING	dehydrogenase	Human Gene Similar to SPTREMBL-ID:Q23612 SIMILAR TO SHORT-CHAIN ALCOHOL DEHYDROGENASE. NCBI GI: 1086671 - CAENORHABDITIS ELEGANS, 325 aa.	3.70E-51	14
1369	cg43918191	229	GGCTGCTGTTTC ACTGAGACAGGA C[G/A]AACCACCA AGTCCAAATGAG AAGAC	G	A		SILENT-NONCODING	dehydrogenase	Human Gene Similar to SPTREMBL-ID:Q23612 SIMILAR TO SHORT-CHAIN ALCOHOL DEHYDROGENASE. NCBI GI: 1086671 - CAENORHABDITIS ELEGANS, 325 aa.	3.70E-51	14

1370	cg43979957	133	ACTTTATTAAAGTTACTTTTCCAGA[G/A]AATTCAGTAAATATGGTAATATAGG	G	A			SILENT-NONCODING	dehydrogenase	Human Gene Similar to SPTREMBL-ID:Q29259 NADH DEHYDROGENASE (UBIQUINONE) - SUS SCROFA (PIG), 128 aa (fragment).	4.00E-50	9
1371	cg43937259	397	CCCCCTGGAAAGTGATCCCGGCATC[C/G]GAGAGCCAAGATGCCGGCCCCACTTG	C	G			SILENT-NONCODING	desaturase	Human Gene SWISSPROT-ID:O00767 ACYL-COA DESATURASE (EC 1.14.99.5) (STEAROYL-COA DESATURASE) (FATTY ACID DESATURASE) (DELTA(9)-DESATURASE) - HOMO SAPIENS (HUMAN), 359 aa.\|pcls:SPTREMBL-ID:O00767 ACYL-COA DESATURASE 1 (EC 1.14.99.5) (STEAROYL-COA DESATURASE 1) (FATTY ACID DESATURASE 1) - HOMO SAPIENS (HUMAN), 359 aa.	8.10E-194	
1372	cg44000579	1236	CTTACAGCCATTTCCTGAATGGCTG[gap/C]TGCGCTTTCCCTCTGTCATCTCCTT	gap	C			SILENT-NONCODING	desaturase	Human Gene Homologous to SPTREMBL-ID:O00119 FUNGAL STEROL-C5-DESATURASE HOMOLOG HOMO SAPIENS (HUMAN), 236 aa.	6.20E-128	20
1373	cg44000579	47	CGCCGACCTTTTTTTTTTTTT[T/A]TTTTAATTATGATCAACTTTTATTG	T	A			SILENT-NONCODING	desaturase	Human Gene Homologous to SPTREMBL-ID:O00119 FUNGAL STEROL-C5-DESATURASE HOMOLOG HOMO SAPIENS (HUMAN), 236 aa.	6.20E-128	20
1374	cg43291836	264	TCTAAAGTGCCAGTATTATTTACAC[T/gap]TTTTTTTTTTTTTAGCCAAAAGTC	T	gap			SILENT-NONCODING	dna_rna_bind	Human Gene TREMBLNEW-ID:G2828110 ZINC FINGER DNA BINDING PROTEIN 89 KDA - HOMO SAPIENS (HUMAN), 794 aa.	0.00E+00	3
1375	cg40993080	282	AAGTTTATTTGGTATCTTTGGAAAG[gap/G]AAATTATAAAGATTCGTCTGGGAAA	gap	G			SILENT-NONCODING	dna_rna_bind	Human Gene SWISSPROT-ID:P21580 TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 3 (PUTATIVE DNA BINDING PROTEIN A20) (ZINC FINGER PROTEIN A20) - HOMO SAPIENS (HUMAN), 790 aa.	0.00E+00	6

1376	cg43926092	37	TTTTTTTTTTTTTT[T/A]TTTTTTCTTCTTATATTCTACTTTAT	T	A		SILENT-NONCODING	dna_rna_bind	Human Gene SWISSPROT-ID:P33194 POSSIBLE DNA-REPAIR PROTEIN XP-E (POSSIBLE XERODERMA PIGMENTOSUM GROUP E PROTEIN) (UV-DAMAGED DNA-BINDING PROTEIN) (UV-DDB) - CERCOPITHECUS AETHIOPS (GREEN MONKEY) (GRIVET), 1140 aa.	0.00E+00	11 (11q12)
1377	cg43962927	198	GATGCTGAGGCTGTGGGGCAGCTTT[gap/T]CCCGGGACAACCACGTGGGAGAGCC	gap	T		SILENT-NONCODING	dna_rna_bind	Human Gene SWISSPROT-ID:P38935 DNA-BINDING PROTEIN SMUBP-2 (GLIAL FACTOR-1) (GF-1) - HOMO SAPIENS (HUMAN), 993 aa.	0.00E+00	11 (11q13.2)
1378	cg43962927	208	GCTGTGGGGCAGCTTTCCCGGGACA[A/G]CCACGTGGGAGAGCCGGCTCACCTG	A	G		SILENT-NONCODING	dna_rna_bind	Human Gene SWISSPROT-ID:P38935 DNA-BINDING PROTEIN SMUBP-2 (GLIAL FACTOR-1) (GF-1) - HOMO SAPIENS (HUMAN), 993 aa.	0.00E+00	11 (11q13.2)
1379	cg43962927	224	CCCGGGACAACCACGTGGGAGAGCC[G/A]GCTCACCTGGTCCCCACGGTGAGGC	G	A		SILENT-NONCODING	dna_rna_bind	Human Gene SWISSPROT-ID:P38935 DNA-BINDING PROTEIN SMUBP-2 (GLIAL FACTOR-1) (GF-1) - HOMO SAPIENS (HUMAN), 993 aa.	0.00E+00	11 (11q13.2)
1380	cg43962927	264	CACGGTGAGGCGCAACAAGGAGGGG[C/T]TGGCACAGGCCAGGCACCTTTATAA	C	T		SILENT-NONCODING	dna_rna_bind	Human Gene SWISSPROT-ID:P38935 DNA-BINDING PROTEIN SMUBP-2 (GLIAL FACTOR-1) (GF-1) - HOMO SAPIENS (HUMAN), 993 aa.	0.00E+00	11 (11q13.2)
1381	cg43962927	612	ACCTTCCCCAGGATCCAGAGGCTGG[A/G]GTGTGGTTTTGGGCGGGGAGTGAGG	A	G		SILENT-NONCODING	dna_rna_bind	Human Gene SWISSPROT-ID:P38935 DNA-BINDING PROTEIN SMUBP-2 (GLIAL FACTOR-1) (GF-1) - HOMO SAPIENS (HUMAN), 993 aa.	0.00E+00	11 (11q13.2)

1382	cg43962927	613	CCTTCCCCAGGA TCCAGAGGCTG GA[G/A]TGTGGTT TTGGGCGGGGA GTGAGGG	G	A			SILENT-NONCODING	dna_rna_bind	Human Gene SWISSPROT-ID:P38935 DNA-BINDING PROTEIN SMUBP-2 (GLIAL FACTOR-1) (GF-1) - HOMO SAPIENS (HUMAN), 993 aa.	0.00E+00	11 (11q13.2)
1383	cg43962927	634	TGGAGTGTGGTT TTGGGCGGGGA GT[G/A]AGGGGA AGGGACGTGCAT TTCCCAA	G	A			SILENT-NONCODING	dna_rna_bind	Human Gene SWISSPROT-ID:P38935 DNA-BINDING PROTEIN SMUBP-2 (GLIAL FACTOR-1) (GF-1) - HOMO SAPIENS (HUMAN), 993 aa.	0.00E+00	11 (11q13.2)
1384	cg43968816	1025	TTCTGAGATGCG CACGAGGGAGG AA[A/gap]TTGCTT AGTCCACCATCA AGAGCCT	A	gap			SILENT-NONCODING	dna_rna_bind	Human Gene SWISSPROT-ID:P27694 REPLICATION PROTEIN A 70 KD DNA-BINDING SUBUNIT (RP-A) (RF-A) (REPLICATION FACTOR-A PROTEIN 1) (SINGLE-STRANDED DNA-BINDING PROTEIN) - HOMO SAPIENS (HUMAN), 616 aa.	0.00E+00	17 (17p13.3)
1385	cg43968816	357	TAGCTTTAGTCA AAAAAAACAAAA T[A/G]CATGAATG CAGGAATGTGTA CAGGT	A	G			SILENT-NONCODING	dna_rna_bind	Human Gene SWISSPROT-ID:P27694 REPLICATION PROTEIN A 70 KD DNA-BINDING SUBUNIT (RP-A) (RF-A) (REPLICATION FACTOR-A PROTEIN 1) (SINGLE-STRANDED DNA-BINDING PROTEIN) - HOMO SAPIENS (HUMAN), 616 aa.	0.00E+00	17 (17p13.3)
1386	cg43968816	431	CGAAGCGCAGC ATTAATTGAAGT GA[A/G]AAGTAAA GAAACGCTTTGT AGCCGC	A	G			SILENT-NONCODING	dna_rna_bind	Human Gene SWISSPROT-ID:P27694 REPLICATION PROTEIN A 70 KD DNA-BINDING SUBUNIT (RP-A) (RF-A) (REPLICATION FACTOR-A PROTEIN 1) (SINGLE-STRANDED DNA-BINDING PROTEIN) - HOMO SAPIENS (HUMAN), 616 aa.	0.00E+00	17 (17p13.3)
1387	cg43968816	476	AGCCGCTCGGAT TTCCTTAGGGGA C[A/G]GCAAGTC AATGCTTATCAG CGGTCC	A	G			SILENT-NONCODING	dna_rna_bind	Human Gene SWISSPROT-ID:P27694 REPLICATION PROTEIN A 70 KD DNA-BINDING SUBUNIT (RP-A) (RF-A) (REPLICATION FACTOR-A PROTEIN 1) (SINGLE-STRANDED DNA-BINDING PROTEIN) - HOMO SAPIENS (HUMAN), 616 aa.	0.00E+00	17 (17p13.3)

1388	cg43968816	482	TCGGATTTCCTTAGGGGACAGCAAG[T/A]CAATGCTTATCAGCGGTCCTCAGAA	T	A			SILENT-NONCODING	dna_rma_bind	Human Gene SWISSPROT-ID:P27694 REPLICATION PROTEIN A 70 KD DNA-BINDING SUBUNIT (RP-A) (RF-A) (REPLICATION FACTOR-A PROTEIN 1) (SINGLE-STRANDED DNA-BINDING PROTEIN) - HOMO SAPIENS (HUMAN), 616 aa.	0.00E+00	17 (17p13.3)
1389	cg43968816	555	GACCCATCTGACTCAGTCTATTAAA[C/G]CCTGAAGGAAGGATACTCTTCAGAT	C	G			SILENT-NONCODING	dna_rma_bind	Human Gene SWISSPROT-ID:P27694 REPLICATION PROTEIN A 70 KD DNA-BINDING SUBUNIT (RP-A) (RF-A) (REPLICATION FACTOR-A PROTEIN 1) (SINGLE-STRANDED DNA-BINDING PROTEIN) - HOMO SAPIENS (HUMAN), 616 aa.	0.00E+00	17 (17p13.3)
1390	cg44129390	4713	CACCAATACACATAAATGGGGGAG[gap/A]AAAGCTATGAAACTGTATAGGGCTG	gap	A			SILENT-NONCODING	dna_rma_bind	Human Gene SWISSNEW-ID:P52701 DNA MISMATCH REPAIR PROTEIN MSH6 (MUTS-ALPHA 160 KD SUBUNIT) (G/T MISMATCH BINDING PROTEIN) (GTBP) (GTMBP) (P160) - HOMO SAPIENS (HUMAN), 1360 aa. aa.\|pcls:SWISSPROT-ID:P52701 DNA MISMATCH REPAIR PROTEIN MSH6 (MUTS-ALPHA 160 KD SUBUNIT) (G/T MISMATCH BINDING PROTEIN) (GTBP) (GTMBP) (P160) - HOMO SAPIENS (HUMAN), 1360 aa.	0.00E+00	2 (2p16)
1391	cg44129390	4716	CAATACACATAAATGGGGGAGGAAA[gap/A]GCTATGAAACTGTATAGGGCTGTAT	gap	A			SILENT-NONCODING	dna_rma_bind	Human Gene SWISSNEW-ID:P52701 DNA MISMATCH REPAIR PROTEIN MSH6 (MUTS-ALPHA 160 KD SUBUNIT) (G/T MISMATCH BINDING PROTEIN) (GTBP) (GTMBP) (P160) - HOMO SAPIENS (HUMAN), 1360 aa. aa.\|pcls:SWISSPROT-ID:P52701 DNA MISMATCH REPAIR PROTEIN MSH6 (MUTS-ALPHA 160 KD SUBUNIT) (G/T MISMATCH BINDING PROTEIN) (GTBP) (GTMBP) (P160) - HOMO SAPIENS (HUMAN), 1360 aa.	0.00E+00	2 (2p16)

1392	cg44129390	5268	TCTGAATACATG TTAAAAAAAAAAA [A/gap]TCAAAAG GAACGCAGAAGT GCTAGC	A	gap		SILENT-NONCODING	dna_rma_bind	Human Gene SWISSNEW-ID:P52701 DNA MISMATCH REPAIR PROTEIN MSH6 (MUTS-ALPHA 160 KD SUBUNIT) (G/T MISMATCH BINDING PROTEIN) (GTBP) (P160) - HOMO SAPIENS (HUMAN), 1360 aa.\|pcls:SWISSPROT-ID:P52701 DNA MISMATCH REPAIR PROTEIN MSH6 (MUTS-ALPHA 160 KD SUBUNIT) (G/T MISMATCH BINDING PROTEIN) (GTBP) (P160) - HOMO SAPIENS (HUMAN), 1360 aa.	0.00E+00	2 (2p16)
1393	cg44005808	3654	CGTGTAAACCAA AGCCCTAAAATT C[C/gap]ACTGCG TTGTCCACAAGA CAGAAGC	C	gap		SILENT-NONCODING	dna_rma_bind	Human Gene SWISSNEW-ID:P19838 NUCLEAR FACTOR NF-KAPPA-B P105 SUBUNIT (DNA-BINDING FACTOR KBF1) (EBP- 1) [CONTAINS: NUCLEAR FACTOR NF-KAPPA-B P50 SUBUNIT] - HOMO SAPIENS (HUMAN), 969 aa.\|pcls:SWISSPROT-ID:P19838 NUCLEAR FACTOR NF-KAPPA-B P105 SUBUNIT (CONTAINS: NUCLEAR FACTOR NF- KAPPA-B P50 SUBUNIT) (DNA-BINDING FACTOR KBF1) (EBP-1) HOMO SAPIENS (HUMAN), 969 aa.	0.00E+00	
1394	cg44005808	3835	ATCTAGCAATCA CAACACTGGCTG A[G/A]CGGATGC ATCTGGGGATGA GGTTGC	G	A		SILENT-NONCODING	dna_rma_bind	Human Gene SWISSNEW-ID:P19838 NUCLEAR FACTOR NF-KAPPA-B P105 SUBUNIT (DNA-BINDING FACTOR KBF1) (EBP- 1) [CONTAINS: NUCLEAR FACTOR NF-KAPPA-B P50 SUBUNIT] - HOMO SAPIENS (HUMAN), 969 aa.\|pcls:SWISSPROT-ID:P19838 NUCLEAR FACTOR NF-KAPPA-B P105 SUBUNIT (CONTAINS: NUCLEAR FACTOR NF- KAPPA-B P50 SUBUNIT) (DNA-BINDING FACTOR KBF1) (EBP-1) HOMO SAPIENS (HUMAN), 969 aa.	0.00E+00	

1395	cg44005808	3841	CAATCACAACAC TGGCTGAGCGG AT[G/gap]CATCT GGGGATGAGGT TGCTTACTA	G	gap		SILENT-NONCODING	dna_ma_bind	Human Gene SWISSNEW-ID:P19838 NUCLEAR FACTOR NF-KAPPA-B P105 SUBUNIT (DNA-BINDING FACTOR KBF1) (EBP- 1) [CONTAINS: NUCLEAR FACTOR NF-KAPPA-B P50 SUBUNIT] - HOMO SAPIENS (HUMAN), 969 aa.	pdb:SWISSPROT-ID:P19838 NUCLEAR FACTOR NF-KAPPA-B P105 SUBUNIT (CONTAINS: NUCLEAR FACTOR NF- KAPPA-B P50 SUBUNIT) (DNA-BINDING FACTOR KBF1) (EBP-1) HOMO SAPIENS (HUMAN), 969 aa.	0.00E+00	
1396	cg44005808	3962	TATTGTCATTAAA GGTATCACGGTC [G/gap]CCACCTG GCATTCCTTCTG ACCACA	G	gap		SILENT-NONCODING	dna_ma_bind	Human Gene SWISSNEW-ID:P19838 NUCLEAR FACTOR NF-KAPPA-B P105 SUBUNIT (DNA-BINDING FACTOR KBF1) (EBP- 1) [CONTAINS: NUCLEAR FACTOR NF-KAPPA-B P50 SUBUNIT] - HOMO SAPIENS (HUMAN), 969 aa.	pdb:SWISSPROT-ID:P19838 NUCLEAR FACTOR NF-KAPPA-B P105 SUBUNIT (CONTAINS: NUCLEAR FACTOR NF- KAPPA-B P50 SUBUNIT) (DNA-BINDING FACTOR KBF1) (EBP-1) HOMO SAPIENS (HUMAN), 969 aa.	0.00E+00	
1397	cg43258220	4244	AAAATCAGATCC GAGGCTTGTTTT T[T/gap]CCTTGTC TAGATATGTTTTA AAAGA	T	gap		SILENT-NONCODING	dna_ma_bind	Human Gene SPTREMBL-ID:O00425 PUTATIVE RNA BINDING PROTEIN KOC (KOC) - HOMO SAPIENS (HUMAN), 579 aa.	1.30E-300	7	
1398	cg43094267	1953	ACAGAAGAAACT ACGCAAAAAAAG T[G/T]TGAAGTCA TGCAAACTCCTA CTTTA	G	T		SILENT-NONCODING	dna_ma_bind	Human Gene SWISSNEW-ID:Q13422 DNA-BINDING PROTEIN IKAROS (LYMPHOID TRANSCRIPTION FACTOR LYF-1) - HOMO SAPIENS (HUMAN), 519 aa.	5.40E-285	7	

1399	cg43950470	3069	ATTTTAACTTAGAGCTTTTTTTTTT[gap/T]AATTTTGTCTGCCCCAAGTTTTGTG	gap	T			SILENT-NONCODING	dna_rna_bind	Human Gene SPTREMBL-ID:P70568 RNA BINDING PROTEIN - RATTUS NORVEGICUS (RAT), 550 aa (fragment).	2.00E-271	X (Xq27.3)
1400	cg43931615	417	AGACACCTGAGCTCACTGGTGAACT[C/T]TGCTTCAAGTCCTCCTGCAAAGCAC	C	T			SILENT-NONCODING	dna_rna_bind	Human Gene SPTREMBL-ID:Q13148 TAR DNA-BINDING PROTEIN-43 - HOMO SAPIENS (HUMAN), 414 aa.	4.30E-227	20
1401	cg43931615	832	TTTCTCGCTCATACTAGCCTTTCAT[G/gap]CCTCGGCACCACCATCAATCCCACA	G	gap			SILENT-NONCODING	dna_rna_bind	Human Gene SPTREMBL-ID:Q13148 TAR DNA-BINDING PROTEIN-43 - HOMO SAPIENS (HUMAN), 414 aa.	4.30E-227	20
1402	cg43962830	137	TCTTCTGATCACAGATGGAGTGGAA[A/T]GAGTTGAAAATGCCTTCTAGAATCC	A	T			SILENT-NONCODING	dna_rna_bind	Human Gene TREMBLNEW-ID:G2801552 RNA BINDING PROTEIN ELAVL4 - MUS MUSCULUS (MOUSE), 346 aa.	2.90E-184	1 (1p34)
1403	cg43956159	1034	CATCTCATCTCATGGTATACTCCTT[A/T]CACACAAAACATTCAAACTACTTTT	A	T			SILENT-NONCODING	dna_rna_bind	Human Gene SPTREMBL-ID:Q99612 DNA-BINDING PROTEIN CPBP - HOMO SAPIENS (HUMAN), 290 aa (fragment).	1.40E-159	10
1404	cg43956159	1175	AACCATTAGCATTCTCAGTGTGCAT[G/gap]CTCACGGCAAAGGCTTAGGCGCCGC	G	gap			SILENT-NONCODING	dna_rna_bind	Human Gene SPTREMBL-ID:Q99612 DNA-BINDING PROTEIN CPBP - HOMO SAPIENS (HUMAN), 290 aa (fragment).	1.40E-159	10
1405	cg43956159	1195	GCATGCTCACGGCAAAGGCTTAGGC[gap/C]GCCGCTCGGAAGGGCGGGTACCAGT	gap	C			SILENT-NONCODING	dna_rna_bind	Human Gene SPTREMBL-ID:Q99612 DNA-BINDING PROTEIN CPBP - HOMO SAPIENS (HUMAN), 290 aa (fragment).	1.40E-159	10

1406	cg43956159	1250	GTCCAGGGTCACCCACATACCATGC[gap/C]ACCACGGGTGCTATGCCGCTTCTTA	gap	C			SILENT-NONCODING	dna_rna_bind	Human Gene SPTREMBL-ID:Q99612 DNA-BINDING PROTEIN CPBP - HOMO SAPIENS (HUMAN), 290 aa (fragment).	1.40E-159	10
1407	cg43971682	415	TTTTTGTCTTTATTGACTTTATTTT[gap/T]AGTTTTTGTACATAAAGAAAAATCA	gap	T			SILENT-NONCODING	dna_rna_bind	Human Gene SWISSPROT-ID:P52912 NUCLEOLYSIN TIA-1 (RNA BINDING PROTEIN TIA-1) - MUS MUSCULUS (MOUSE), 386 aa.	6.10E-157	
1408	cg43917883	2776	TGTTTGGAACAGGAGAATTTTTTTT[T/gap]CCTTTTTATTTCTTTATTTTTTCTT	T	gap			SILENT-NONCODING	dna_rna_bind	Human Gene Homologous to SWISSPROT-ID:Q15233 54 KD NUCLEAR RNA-BINDING PROTEIN (P54(NRB)) - HOMO SAPIENS (HUMAN), 471 aa.	2.70E-138	1
1409	cg43917883	2884	CAAAGTGTACCAATTTTTTTTTTTT[T/gap]ACTGTGCTTCAAATAAATAGAAAAA	T	gap			SILENT-NONCODING	dna_rna_bind	Human Gene Homologous to SWISSPROT-ID:Q15233 54 KD NUCLEAR RNA-BINDING PROTEIN (P54(NRB)) - HOMO SAPIENS (HUMAN), 471 aa.	2.70E-138	1
1410	cg43917883	3009	CATGAGAGTGTCTAGGCCTTTGAAT[G/gap]GCATATGCCATTTCTGGGAAATGCA	G	gap			SILENT-NONCODING	dna_rna_bind	Human Gene Homologous to SWISSPROT-ID:Q15233 54 KD NUCLEAR RNA-BINDING PROTEIN (P54(NRB)) - HOMO SAPIENS (HUMAN), 471 aa.	2.70E-138	1
1411	cg43917883	555	GCGGCCTCCACGACTTCCGTTCTCC[C/gap]GCCGCCCGGCATGGGCCTCAATCAG	C	gap			SILENT-NONCODING	dna_rna_bind	Human Gene Homologous to SWISSPROT-ID:Q15233 54 KD NUCLEAR RNA-BINDING PROTEIN (P54(NRB)) - HOMO SAPIENS (HUMAN), 471 aa.	2.70E-138	1
1412	cg43967456	1506	CATTCGTTCATTCCTGGCTATCTAG[gap/A]AAAAAAAAGTCAGTGGTATGCCTT	gap	A			SILENT-NONCODING	dna_rna_bind	Human Gene Homologous to SWISSPROT-ID:Q15233 54 KD NUCLEAR RNA-BINDING PROTEIN (P54(NRB)) - HOMO SAPIENS (HUMAN), 471 aa.	1.90E-137	

1413	cg43967456	1515	ATTCCTGGCTATCTAGAAAAAAAAA[gap/A]GTCAGTGGTATGCCTTTATACTTTT	gap	A			SILENT-NONCODING	dna_rna_bind	Human Gene Homologous to SWISSPROT-ID:Q15233 54 KD NUCLEAR RNA-BINDING PROTEIN (P54(NRB)) - HOMO SAPIENS (HUMAN), 471 aa.	1.90E-137	
1414	cg43967456	1523	GCTATCTAGAAAAAAAAAGTCAGTG[G/A]TATGCCTTTATACTTTTACCTGTTA	G	A			SILENT-NONCODING	dna_rna_bind	Human Gene Homologous to SWISSPROT-ID:Q15233 54 KD NUCLEAR RNA-BINDING PROTEIN (P54(NRB)) - HOMO SAPIENS (HUMAN), 471 aa.	1.90E-137	
1415	cg43967456	1593	TTGTTAATGTATGTAGACTTAAAAG[T/gap]TTTTTTTTTTTGTAAAACTTGAGGT	T	gap			SILENT-NONCODING	dna_rna_bind	Human Gene Homologous to SWISSPROT-ID:Q15233 54 KD NUCLEAR RNA-BINDING PROTEIN (P54(NRB)) - HOMO SAPIENS (HUMAN), 471 aa.	1.90E-137	
1416	cg43967456	1604	GTAGACTTAAAAGTTTTTTTTTTTT[gap/T]GTAAAACTTGAGGTTTTTGTATTTT	gap	T			SILENT-NONCODING	dna_rna_bind	Human Gene Homologous to SWISSPROT-ID:Q15233 54 KD NUCLEAR RNA-BINDING PROTEIN (P54(NRB)) - HOMO SAPIENS (HUMAN), 471 aa.	1.90E-137	
1417	cg43967456	1751	TAGTACTGTGAAATCTATGTAGTTA[gap/A]ATCTCAATAAAGAAATCATTTTGGA	gap	A			SILENT-NONCODING	dna_rna_bind	Human Gene Homologous to SWISSPROT-ID:Q15233 54 KD NUCLEAR RNA-BINDING PROTEIN (P54(NRB)) - HOMO SAPIENS (HUMAN), 471 aa.	1.90E-137	
1418	cg44031794	336	CCGATCTCAGCCTTGCTGATCATCT[C/T]GTACAGCAGCAGAAAATGACCATGT	C	T			SILENT-NONCODING	dna_rna_bind	Human Gene Homologous to SPTREMBL-ID:Q61491 DNA-BINDING PROTEIN - MUS MUSCULUS (MOUSE), 546 aa.	2.40E-137	5
1419	cg43930612	629	GAGGTAGAGCGGGCGCGCGGCAGCG[G/gap]CGGGGATTACTTTGCTGCTAGTTTC	G	gap			SILENT-NONCODING	dna_rna_bind	Human Gene Homologous to SPTREMBL-ID:Q60668 ARE ELEMENT RNA-BINDING PROTEIN AUF1 - MUS MUSCULUS (MOUSE), 269 aa.	1.30E-134	4 (4q21.1)

1420	cg43930612	668	GCTGCTAGTTTCGGTTCGCGGCAGC[G/gap]GCGGGTGTAGTCTCGGCGGCAGCGG	G	gap			SILENT-NONCODING	dna_rna_bind	Human Gene Homologous to SPTREMBL-ID:Q60668 ARE ELEMENT RNA-BINDING PROTEIN AUF1 - MUS MUSCULUS (MOUSE), 269 aa.	1.30E-134	4 (4q21.1)
1421	cg43933275	1461	AGCACCACCTGCCTCTGGGAATAGG[G/gap]CTCACCCGCGCCGAGAGGTCTGGAG	G	gap			SILENT-NONCODING	dna_rna_bind	Human Gene Homologous to SPTREMBL-ID:Q64012 MERC=RNA-BINDING PROTEIN {ALTERNATIVELY SPLICED, EXON 1AY} - MUS MUSCULUS (MOUSE), 296 aa.	1.20E-131	20
1422	cg43933275	256	GGGGAGGGGAGGTAGTATGGGGAAA[C/gap]CCCTGTGCTCTACCCTCTGGCCTGG	C	gap			SILENT-NONCODING	dna_rna_bind	Human Gene Homologous to SPTREMBL-ID:Q64012 MERC=RNA-BINDING PROTEIN {ALTERNATIVELY SPLICED, EXON 1AY} - MUS MUSCULUS (MOUSE), 296 aa.	1.20E-131	20
1423	cg43281802	290	GAGATTTCTTTTTCCAGGCCCAGGC[C/gap]TGTGAAAAACGATGGCTAAGTGTTA	C	gap			SILENT-NONCODING	dna_rna_bind	Human Gene Homologous to SWISSPROT-ID:P29558 SINGLE-STRANDED DNA-BINDING PROTEIN MSSP-1 - HOMO SAPIENS (HUMAN), 372 aa.	1.30E-122	12
1424	cg43935457	728	CAGAACTGGTTTCTTTTTTTTTTTT[T/gap]CAAGTTTTAGAGAACTAAATTTGCA	T	gap			SILENT-NONCODING	dna_rna_bind	Human Gene Homologous to SPTREMBL-ID:Q62262 SPERMATID PERINUCLEAR RNA BINDING PROTEIN - MUS MUSCULUS (MOUSE), 648 aa.	6.00E-118	
1425	cg43973273	1019	CCATGGAAATGATAAGGAATCAAAT[G/T]TTCTGCATCAGTAATTTTAATAAAG	G	T			SILENT-NONCODING	dna_rna_bind	Human Gene Homologous to SPTREMBL-ID:Q13097 DNA/RNA-BINDING PROTEIN - HOMO SAPIENS (HUMAN), 363 aa (fragment).	2.00E-112	

1426	cg43955901	20	TTTTTTTTTTTTT TTTTAT[G/T]TTT GTAAATTTTACTT AGGCCATCA	G	T		SILENT-NONCODING	dna_ma_bind	Human Gene Similar to SWISSNEW-ID:Q91836 DOUBLE STRANDED RNA BINDING PROTEIN A (XLRBPA) - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 298 aa.\|pcls:SWISSPROT-ID:Q91836 DOUBLE STRANDED RNA BINDING PROTEIN A - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 298 aa.\|pcls:SPTREMBL-ID:Q91836 RNA BINDING PROTEIN - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 298 aa.	9.40E-97	2
1427	cg43955901	24	TTTTTTTTTTTTT TTTTATGTTT[G/T]TAAATTTTACTT AGGCCATCATTT T	G	T		SILENT-NONCODING	dna_ma_bind	Human Gene Similar to SWISSNEW-ID:Q91836 DOUBLE STRANDED RNA BINDING PROTEIN A (XLRBPA) - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 298 aa.\|pcls:SWISSPROT-ID:Q91836 DOUBLE STRANDED RNA BINDING PROTEIN A - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 298 aa.\|pcls:SPTREMBL-ID:Q91836 RNA BINDING PROTEIN - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 298 aa.	9.40E-97	2
1428	cg44922718	1197	CATACTTATCAA GCAGTTGCAGAT A[A/gap]TGAAAC ATTATCAGCTAT CAATAAT	A	gap		SILENT-NONCODING	dna_ma_bind	Human Gene Similar to TREMBLNEW-ID:G2673961 ASTROCYTIC NOVA-LIKE RNA-BINDING PROTEIN - HOMO SAPIENS (HUMAN), 498 aa (fragment).	1.80E-82	
1429	cg44922718	1251	TTGGCACTTTCA CTTTTGTTTATAA [A/gap]ATTTCCAA TACACTGTACCA CAGTT	A	gap		SILENT-NONCODING	dna_ma_bind	Human Gene Similar to TREMBLNEW-ID:G2673961 ASTROCYTIC NOVA-LIKE RNA-BINDING PROTEIN - HOMO SAPIENS (HUMAN), 498 aa (fragment).	1.80E-82	

1430	cg44922718	1252	TGGCACTTTCACTTTTGTTTATAAA[A/gap]TTTCCAATACACTGTACCACAGTTA	A	gap			SILENT-NONCODING	dna_rna_bind	Human Gene Similar to TREMBLNEW-ID:G2673961 ASTROCYTIC NOVA-LIKE RNA-BINDING PROTEIN - HOMO SAPIENS (HUMAN), 498 aa (fragment).	1.80E-82	
1431	cg44922718	1261	CACTTTTGTTTATAAAATTTCCAAT[A/gap]CACTGTACCACAGTTATGTGTCTAA	A	gap			SILENT-NONCODING	dna_rna_bind	Human Gene Similar to TREMBLNEW-ID:G2673961 ASTROCYTIC NOVA-LIKE RNA-BINDING PROTEIN - HOMO SAPIENS (HUMAN), 498 aa (fragment).	1.80E-82	
1432	cg44922718	1263	CTTTTGTTTATAAAATTTCCAATAC[A/gap]CTGTACCACAGTTATGTGTCTAAAC	A	gap			SILENT-NONCODING	dna_rna_bind	Human Gene Similar to TREMBLNEW-ID:G2673961 ASTROCYTIC NOVA-LIKE RNA-BINDING PROTEIN - HOMO SAPIENS (HUMAN), 498 aa (fragment).	1.80E-82	
1433	cg44922718	1318	AGGATGTTAATGGAGTAATGACTGT[T/gap]CTACTGGCCAGGCGATGGGATCAGT	T	gap			SILENT-NONCODING	dna_rna_bind	Human Gene Similar to TREMBLNEW-ID:G2673961 ASTROCYTIC NOVA-LIKE RNA-BINDING PROTEIN - HOMO SAPIENS (HUMAN), 498 aa (fragment).	1.80E-82	
1434	cg44922718	1356	CGATGGGATCAGTAGTGAATTCAGT[G/gap]CTTAAAAACAAATGTACAAACCTCT	G	gap			SILENT-NONCODING	dna_rna_bind	Human Gene Similar to TREMBLNEW-ID:G2673961 ASTROCYTIC NOVA-LIKE RNA-BINDING PROTEIN - HOMO SAPIENS (HUMAN), 498 aa (fragment).	1.80E-82	
1435	cg44922718	1372	GAATTCAGTGCTTAAAAACAAATGT[A/G]CAAACCTCTGAAGAGGTGGGACTCC	A	G			SILENT-NONCODING	dna_rna_bind	Human Gene Similar to TREMBLNEW-ID:G2673961 ASTROCYTIC NOVA-LIKE RNA-BINDING PROTEIN - HOMO SAPIENS (HUMAN), 498 aa (fragment).	1.80E-82	
1436	cg44922718	1376	TCAGTGCTTAAAAACAAATGTACAA[A/gap]CCTCTGAAGAGGTGGGACTCCATGT	A	gap			SILENT-NONCODING	dna_rna_bind	Human Gene Similar to TREMBLNEW-ID:G2673961 ASTROCYTIC NOVA-LIKE RNA-BINDING PROTEIN - HOMO SAPIENS (HUMAN), 498 aa (fragment).	1.80E-82	